

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 09:28:25 ; Search time 225 Seconds
(without alignment)
7931.875 Million cell updates/sec

Title: US-10-698-689-85
Perfect score: 1004
Sequence: 1 gctcgcctggggccagtc.....ccagtcagtcgacgcccctc 1004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/1 COMB.seq:
2: /cgn2_6/ptodata/1/ina/5 COMB.seq:
3: /cgn2_6/ptodata/1/ina/6 COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:
5: /cgn2_6/ptodata/1/ina/H COMB.seq:
6: /cgn2_6/ptodata/1/ina/PCRB COMB.seq:
7: /cgn2_6/ptodata/1/ina/PP COMB.seq:
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:
9: /cgn2_6/ptodata/1/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	50	5.0	50	US-10-131-827-108
2	50	5.0	50	US-10-131-827-2096
3	28	2.8	28	US-08-859-998-471
C 4	28	2.8	28	US-08-859-998-472
5	28	2.8	28	US-09-225-928-471
C 6	28	2.8	28	US-09-225-928-472
7	28	2.8	28	US-09-225-201B-471
C 8	28	2.8	28	US-09-225-201B-472
9	25	2.5	25	US-09-071-433-88
10	25	2.5	25	US-09-344-260A-14
11	25	2.5	25	US-09-396-196G-44613
12	25	2.5	25	US-09-396-196G-44614
13	25	2.5	25	US-09-396-196G-44615
14	25	2.5	25	US-09-396-196G-44616
15	25	2.5	25	US-09-396-196G-44617
16	25	2.5	25	US-09-396-196G-44618
17	25	2.5	25	US-09-396-196G-44619
18	25	2.5	25	US-09-396-196G-44620
19	25	2.5	25	US-09-396-196G-44621
20	25	2.5	25	US-09-396-196G-44622
21	25	2.5	25	US-09-396-196G-44623
22	25	2.5	25	US-09-396-196G-44624
23	25	2.5	25	US-09-396-196G-44625
24	25	2.5	25	US-09-396-196G-44626

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c 98      19      1.9      40      2      US-08-484-624A-7      Sequence 7, Appli
c 99      19      1.9      40      2      US-08-477-733B-7      Sequence 7, Appli
c 100     19      1.9      40      3      US-09-088-913A-7      Sequence 7, Appli
c 101     19      1.9      40      3      US-08-769-819-7      Sequence 7, Appli
c 102     19      1.9      40      3      US-08-770-974-7      Sequence 7, Appli
c 103     19      1.9      40      3      US-08-770-981-7      Sequence 7, Appli
c 104     19      1.9      40      3      US-09-399-106-7      Sequence 7, Appli
c 105     19      1.9      47      3      US-09-422-978-2564      Sequence 2564, Ap
c 106     19      1.9      50      3      US-08-985-162-1647      Sequence 1647, Ap
c 107     19      1.9      50      3      US-09-401-063-1647      Sequence 1647, Ap
c 108     18.8    1.9      24      3      US-08-697-610-4        Sequence 4, Appli
c 109     18.8    1.9      24      3      US-08-349-357-4        Sequence 4, Appli
c 110     18.8    1.9      25      3      US-09-396-196G-83409      Sequence 83409, A
c 111     18.8    1.9      41      3      US-08-954-210-68        Sequence 68, Appl
c 112     18.8    1.9      41      3      US-09-431-419A-68        Sequence 68, Appl
c 113     18.8    1.9      46      3      US-10-191-540-98        Sequence 98, Appl
c 114     18.8    1.9      47      3      US-09-641-638-961        Sequence 961, App
c 115     18.8    1.9      47      3      US-09-641-638-1257        Sequence 1257, Ap
c 116     18.8    1.9      47      3      US-09-422-978-213        Sequence 213, App
c 117     18.8    1.9      47      3      US-09-422-978-2304        Sequence 2304, Ap
c 118     18.8    1.9      47      3      US-10-170-097-961        Sequence 961, App
c 119     18.8    1.9      47      3      US-10-170-097-1257        Sequence 1257, Ap
c 120     18.8    1.9      48      2      US-08-487-811A-23        Sequence 23, Appli
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ALIGNMENTS

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RESULT 1
US-10-131-827-108
; Sequence 108, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-108
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Query Match      5.0%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      827      GGTCCACCAGGAGTGGCAAGAGAGTGCATCTCAGTCGAGAGAGAC      876
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Db      1      GGTCCACCAGGAGTGGCAAGAGAGTGCATCTCAGTCGAGAGAGAC      50
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RESULT 2
US-10-131-827-2096
; Sequence 2096, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
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; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2096

Query Match      5.0%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      834      CAGGAGGATGGCAAGAGAGTGCATCTCAGTCGAGAGAGACAGTGAGG      883
      |||||||
Db      1      CAGGAGGATGGCAAGAGAGTGCATCTCAGTCGAGAGAGACAGTGAGG      50
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RESULT 3
US-08-859-998-471
; Sequence 471, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-471
```

Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL EXPRESSION

NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025

STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:

CUONIRI: OS
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER:
APPLICATION NUMBER: US/09/225,328
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620

REFERENCE/DOCKET NUMBER: 09096/0020001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-322-5070
 TELEFAX: 415-854-0875
 INFORMATION FOR SEQ ID NO: 471:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA

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; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 471:
US-09-225-928-471

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Query Match	2.8%;	Score 28;	DB 3;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 96;		
Matches	28;	Conservative	0;	Mismatches 0; Indels
QY	198	TGCACAGAGTTCAC	TGAAACGGAATGCC	225
Db	1	TGCACAGAGTTCAC	TGAAACGGAATGCC	28

OTHER INFORMATION: oligonucleotide primer
US-08-859-998-472

APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION

EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US

RESULT 5
US-09-225-928-471

COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

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; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 472:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 472:
US-09-225-928-472
Query Match          2.8%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 577 CAGGCACAAACAGACTGATGTTGTCG 604
| | | | | | | | | | | | | | | | | |
Db 28 CAGGCACAAACAGACTGATGTTGTCG 1

RESULT 7
US-09-225-201B-471
; Sequence 471, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;           Johhadze, George
;           Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                 EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
```

```
;
; INFORMATION FOR SEQ ID NO: 471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 471:
US-09-225-201B-471
Query Match          2.8%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 TGCACAGGTTCACTGAAACGGAATGCC 225
| | | | | | | | | | | | | | | | | |
Db 1 TGCACAGGTTCACTGAAACGGAATGCC 28

RESULT 8
US-09-225-201B-472/c
; Sequence 472, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;           Johhadze, George
;           Bibilashvilli, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                 EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 472:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 472:
US-09-225-201B-472
Query Match          2.8%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 577 CAGGCACAAACAAGACTGATGTTGCTG 604
Db 28 CAGGCACAAACAAGACTGATGTTGCTG 1

RESULT 9

US-09-071-433-88
; Sequence 88, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsert, Lex M
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071,433A
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-071-433-88

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGGTGAAGCGAATTCCT 250
Db 1 TTCCTTGGGTGAAGCGAATTCCT 25

RESULT 10

US-09-344-260A-14
; Sequence 14, Application US/09344260A
; Patent No. 6576752
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Virta, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS-3508
; CURRENT APPLICATION NUMBER: US/09/344,260A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576752el Sequence
US-09-344-260A-14

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGGTGAAGCGAATTCCT 250
Db 1 TTCCTTGGGTGAAGCGAATTCCT 25

RESULT 11

US-09-396-196G-44613

; Sequence 44613, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44613

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGGTTGCTGCTCTGCAGTGG 72
Db 1 ATGGTTGCTGCTCTGCAGTGG 25

RESULT 12

US-09-396-196G-44614
; Sequence 44614, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44614

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 CGTCTGCTCTGCAGTGGTCTCT 78
Db 1 CGTCTGCTCTGCAGTGGTCTCT 25

RESULT 13

US-09-396-196G-44615
; Sequence 44615, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1

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; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44615
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44615

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 TTGTGCCAGCAGGACACAGAACTGG 189
Db 1 TTGTGCCAGCAGGACACAGAACTGG 25

RESULT 14
US-09-396-196G-44616
; Sequence 44616, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44616

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 GACTGCACAGAGTTCACTGAAACGG 219
Db 1 GACTGCACAGAGTTCACTGAAACGG 25

RESULT 15
US-09-396-196G-44617
; Sequence 44617, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44617

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 GACTGCACAGAGTTCACTGAAACGG 219
Db 1 GACTGCACAGAGTTCACTGAAACGG 25
```

```
; ORGANISM: mus musculus
US-09-396-196G-44617

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 213 GAAACGGAATGCCTTCCTTCGGGTG 237
Db 1 GAAACGGAATGCCTTCCTTCGGGTG 25

RESULT 16
US-09-396-196G-44618
; Sequence 44618, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44618
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44618

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 219 GAATGCCTTCCTTCGGGTGAAAGCG 243
Db 1 GAATGCCTTCCTTCGGGTGAAAGCG 25

RESULT 17
US-09-396-196G-44619
; Sequence 44619, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44619

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 TGCCTTCCTTCGGGTGAAACGGAAT 246
Db 1 TGCCTTCCTTCGGGTGAAACGGAAT 246
```

Db 1 TGCCTTCTTGGGTGAAGCGAAT 25

RESULT 18

US-09-396-196G-44620
; Sequence 44620, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44620

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-44620

Query Match 2.5%; Score 25; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 240 AGCGAATTCCTAGACACCTGGGACCA 264

Db 1 AGCGAATTCCTAGACACCTGGGACCA 25

RESULT 19

US-09-396-196G-44621

; Sequence 44621, Application US/09396196G

; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44621

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-44621

Query Match 2.5%; Score 25; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 GAATTCCTAGACACCTGGGACACAG 267

Db 1 GAATTCCTAGACACCTGGGACACAG 25

RESULT 20

US-09-396-196G-44622

; Sequence 44622, Application US/09396196G

; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44622

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-44622

Query Match

2.5%; Score 25; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 AGAGAGACACACTGCCACCAGCACA 288

Db 1 AGAGAGACACACTGCCACCAGCACA 25

RESULT 21

US-09-396-196G-44623

; Sequence 44623, Application US/09396196G

; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44623

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-44623

Query Match

2.5%; Score 25; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 CACTGCCACCAGCACAATACTGCG 297

Db 1 CACTGCCACCAGCACAATACTGCG 25

RESULT 22

US-09-396-196G-44624

; Sequence 44624, Application US/09396196G

; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44624

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      276 TGCCACCAGCACAATACTGCGACC 300
Db      1 TGCCACCAGCACAATACTGCGACC 25

RESULT 23
US-09-396-196G-44625
; Sequence 44625, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44625

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      57 CTGCGCTCTGCAGTCGCTCCTCTGGG 81
Db      1 CTGCGCTCTGCAGTCGCTCCTCTGGG 25

RESULT 24
US-09-396-196G-44626
; Sequence 44626, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44626

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      60 CCTCTGCAGTCGCTCCTCTGGGGCT 84
Db      1 CCTCTGCAGTCGCTCCTCTGGGGCT 25

Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      63 CTGCAGTCGCTCCTCTCTGGGGCTGCT 87
Db      1 CTGCAGTCGCTCCTCTCTGGGGCTGCT 25

RESULT 25
US-09-396-196G-44627
; Sequence 44627, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44627

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      63 CTGCAGTCGCTCCTCTCTGGGGCTGCT 87
Db      1 CTGCAGTCGCTCCTCTCTGGGGCTGCT 25

RESULT 26
US-09-396-196G-44628
; Sequence 44628, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44628

Query Match      2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      87 TTGCTGACCGCTGTCCATCCAGAAC 111
Db      1 TTGCTGACCGCTGTCCATCCAGAAC 25

RESULT 27
```


US-09-396-196G-44629
; Sequence 44629, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44629

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CCCACTGCATGCAGAGAAAACAGT 138
|||||
Db 1 CCCACTGCATGCAGAGAAAACAGT 25

RESULT 28
US-09-396-196G-44630
; Sequence 44630, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44630
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44630

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 TACCTAATAAAGTCAGTCGTGTT 162
|||||
Db 1 TACCTAATAAAGTCAGTCGTGTT 25

RESULT 29
US-09-396-196G-44631
; Sequence 44631, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44631

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 AACAGTCAGTCGTCTTTTGCC 171
|||||
Db 1 AACAGTCAGTCGTCTTTTGCC 25

RESULT 30
US-09-396-196G-44632
; Sequence 44632, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44632
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-44632

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 162 TCTTTGTCAGCCAGGACAGAAAC 186
|||||
Db 1 TCTTTGTCAGCCAGGACAGAAAC 25

RESULT 31
US-10-234-764-14
; Sequence 14, Application US/10234764
; Patent No. 6825331
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Vita, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS5089
; CURRENT APPLICATION NUMBER: US/10/234,764
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 09/344,260
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 14
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-234-764-14

Query Match          2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGCGTGAAGCGCAATTCCT 250
      |||||
Db 1 TTCCTTGGCGTGAAGCGCAATTCCT 25

RESULT 32
US-07-910-222B-5
; Sequence 5, Application US/07910222B
; Patent No. 5397703
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: A Method for Generation of Antibodies to
; TITLE OF INVENTION: Cell Surface Molecules
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Oncology Corporation
; STREET: 1400 53rd Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,222B
; FILING DATE: 19920709
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 2255-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 420-3300
; TELEFAX: (510) 658-5470
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Forward Primer for CD40, MR108
US-07-910-222B-5

Query Match          2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGTTGCG 55
      |||||
Db 9 CTGGTCTCACCTCGCCATGTTGCG 32

RESULT 34
US-08-070-158-5
; Sequence 5, Application US/08070158
; Patent No. 5677165
; GENERAL INFORMATION:
; APPLICANT: DE BOER, MARK
; APPLICANT: CONROY, LEAH B.
; TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
; TITLE OF INVENTION: USING ANTI-CD40 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
```

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/070,158
;; FILING DATE: 28-MAY-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McGarrigle, Philip L.
;; REGISTRATION NUMBER: 31,395
;; REFERENCE/DOCKET NUMBER: 0925.003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 601-2718
;; TELEFAX: (510) 655-3542
;; TELEX: n/a
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 32 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-070-158-5

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
|||||
DB 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 35
US-08-200-716-5
; Sequence 5, Application US/08200716
; Patent No. 5747034
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods and Materials for Induction
; TITLE OF INVENTION: of T Cell Anergy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,716
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)
US-08-200-716-5

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
|||||
DB 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 36
US-08-200-716-7
; Sequence 7, Application US/08200716
; Patent No. 5747034
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods and Materials for Induction
; TITLE OF INVENTION: of T Cell Anergy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,716
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-200-716-7

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCCATGGTTTCG 55
|||||
DB 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 37
US-08-015-147-5
; Sequence 5, Application US/08015147
; Patent No. 5869050
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods of Blocking T-Cell
; TITLE OF INVENTION: Activation Using
; TITLE OF INVENTION: Anti-B7 Monoclonal Antibodies

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,147
FILING DATE: 02-FEB-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,222
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 31411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Forward Primer for CD40, MR108
US-08-015-147-5

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTGCCCATGGTTG 55
Db 9 CTGGTCTCACCTGCCCATGGTTG 32

RESULT 38
US-08-015-147-7
Sequence 7, Application US/08015147
Patent No. 5869050
GENERAL INFORMATION:
APPLICANT: de Boer, Mark
APPLICANT: Conroy, Leah B.
TITLE OF INVENTION: Methods of Blocking T-Cell
TITLE OF INVENTION: Activation Using
TITLE OF INVENTION: Anti-B7 Monoclonal Antibodies
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,147
FILING DATE: 02-FEB-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,222
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 31411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Forward Primer for Soluble
INDIVIDUAL ISOLATE: CD40, MR108
US-08-015-147-7

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred.No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTGCCCATGGTTG 55
Db 9 CTGGTCTCACCTGCCCATGGTTG 32

RESULT 39
US-08-469-015-5
Sequence 5, Application US/08469015
Patent No. 6004552
GENERAL INFORMATION:
APPLICANT: DE BOER, MARK
APPLICANT: CONROY, LEAH B.
TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
TITLE OF INVENTION: USING ANTI-CD40 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street, R-440
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,015
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/070,158
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle, Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0925.003

TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-015-5

Query Match 2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTCG 32

RESULT 40

US-08-463-893-5
Sequence 5, Application US/08463893
Patent No. 6056959

GENERAL INFORMATION:
APPLICANT: DE BOER, MARK
CONROY, LEAH B.
TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
USING ANTI-CD40 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street, R-440
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,893
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/070,158
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle, Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0925.003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-463-893-5

Query Match 2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTCG 55

Db 9 CTGGTCTCACCTCGCCATGGTTCG 32

RESULT 41

US-09-504-505-5
Sequence 5, Application US/09504505
Patent No. 6315998

GENERAL INFORMATION:
APPLICANT: DE BOER, MARK
CONROY, LEAH B.
TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
USING ANTI-CD40 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street, R-440
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/504,505
FILING DATE: 15-Feb-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,893
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US/08/070,158
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle, Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0925.003

TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-504-505-5

Query Match 2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTCG 32

RESULT 42

US-09-954-764-5
Sequence 5, Application US/09954764
Patent No. 6899879

GENERAL INFORMATION:
APPLICANT: DE BOER, MARK
CONROY, LEAH B.
TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
USING ANTI-CD40 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION

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; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/954,764
; FILING DATE: 18-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,893
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0925.003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-954-764-5

Query Match          2.4%; Score 24; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGCTCTCACCTGCCCATGGTTGCG 55
Db 9 CTGCTCTCACCTGCCCATGGTTGCG 32

RESULT 43
US-07-910-222B-6/c
; Sequence 6, Application US/07910222B
; Patent No. 5397703
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: A Method for Generation of Antibodies to
; TITLE OF INVENTION: Cell Surface Molecules
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Oncology Corporation
; STREET: 1400 53rd Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,222B
; FILING DATE: 19920709
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
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; REFERENCE/DOCKET NUMBER: 2255-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 420-3300
; TELEFAX: (510) 658-5470
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Backward Primer for CD40, MR112
US-07-910-222B-6

Query Match          2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCAGGAGTGTGG 905
Db 34 GGCTGCACCCACCAGGAGTGTGG 11

RESULT 44
US-08-070-158-6/c
; Sequence 6, Application US/08070158
; Patent No. 5677165
; GENERAL INFORMATION:
; APPLICANT: DE BOER, MARK
; APPLICANT: CONROY, LEAH B.
; TITLE OF INVENTION: METHODS OF BLOCKING B-CELL ACTIVATION
; TITLE OF INVENTION: USING ANTI-CD40 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,158
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0925.003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-070-158-6

Query Match          2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 882 GGCTGCACCCACCCAGGAGTGG 905
Db 34 GGCTGCACCCACCCAGGAGTGG 11

RESULT 45

US-08-200-716-6/c
; Sequence 6, Application US/08200716
; Patent No. 5747034
; GENERAL INFORMATION:
; APPLICANT: de Boer, Mark
; APPLICANT: Conroy, Leah B.
; TITLE OF INVENTION: Methods and Materials for Induction
; TITLE OF INVENTION: of T Cell Anergy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,716
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle, Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-200-716-6

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGG 905
Db 34 GGCTGCACCCACCCAGGAGTGG 11

Search completed: February 5, 2006, 12:22:42
Job time : 226 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 09:35:04 ; Search time 876 Seconds

(without alignments)
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Title: US-10-698-689-85

Perfect score: 1004

Sequence: 1 gctcgctcgggcccgagt.....ccagtcagtcgagccccc 1004

Scoring table: IDENTITY_NUC

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

Database : Published Applications NA Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	5.0	50	6	US-10-131-827-108
2	50	5.0	50	6	Sequence 108, Appl
3	33	3.3	40	3	US-10-131-827-2096
4	33	3.3	40	3	Sequence 2096, Ap
5	33	3.3	40	5	US-09-844-684-1
6	27	2.7	27	9	Sequence 1, Appli
7	27	2.7	27	9	Sequence 1, Appli
8	27	2.7	27	9	Sequence 1, Appli
9	27	2.7	27	9	Sequence 5523, Ap
10	26	2.6	26	9	Sequence 5526, Ap
11	25	2.5	25	3	US-10-708-204-5523
12	25	2.5	25	3	Sequence 88, Appl
13	25	2.5	25	5	US-10-116-325-88
14	25	2.5	25	5	Sequence 88, Appl
15	25	2.5	25	7	US-10-234-764-14
16	25	2.5	25	7	Sequence 14, Appl
17	25	2.5	25	8	US-10-388-263-88
18	25	2.5	25	8	Sequence 88, Appl
19	25	2.5	25	9	Sequence 88, Appl
20	25	2.5	25	9	Sequence 88, Appl
21	25	2.5	25	9	Sequence 88, Appl
22	25	2.5	25	9	Sequence 88, Appl
23	25	2.5	25	9	Sequence 88, Appl

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ALIGNMENTS

RESULT 1
US-10-131-827-108
; Sequence 108, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-108

Query Match 5.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 827 GGTCAACCAGGAGTGGCAAGAGAGTCGCATCTCAGTCAGGAGAGAC 876
Db 1 GGTCAACCAGGAGTGGCAAGAGAGTCGCATCTCAGTCAGGAGAGAC 50

RESULT 2
US-10-131-827-2096
; Sequence 2096, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-108

Query Match 5.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 827 GGTCAACCAGGAGTGGCAAGAGAGTCGCATCTCAGTCAGGAGAGAC 876
Db 1 GGTCAACCAGGAGTGGCAAGAGAGTCGCATCTCAGTCAGGAGAGAC 50

RESULT 3
US-09-844-684-1
; Sequence 1, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT APPLICATION NUMBER: US/09/844,684
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-844-684-1

Query Match 3.3%; Score 33; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 CTGTCATCCAGAACCAACCACCTGCATGCAGAG 129
Db 8 CTGTCATCCAGAACCAACCACCTGCATGCAGAG 40

RESULT 4
US-10-040-244-1
; Sequence 1, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2096
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2096

Query Match 5.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 834 CAGGAGATGGCAAGAGAGTCGCATCTCAGTCAGGAGAGACGTGAGG 883
Db 1 CAGGAGATGGCAAGAGAGTCGCATCTCAGTCAGGAGAGACGTGAGG 50
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; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-040-244-1

Query Match 3.3%; Score 33; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 CTGTCCATCCAGAACCCCACTGCATGCAGAG 129
Db 8 CTGTCCATCCAGAACCCCACTGCATGCAGAG 40

RESULT 5

US-10-693-629-1
; Sequence 1, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-693-629-1

Query Match 3.3%; Score 33; DB 7; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 CTGTCCATCCAGAACCCCACTGCATGCAGAG 129
Db 8 CTGTCCATCCAGAACCCCACTGCATGCAGAG 40

RESULT 6

US-10-708-204-5523
; Sequence 5523, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5523
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5523

Query Match 2.7%; Score 27; DB 9; Length 27;
Best Local Similarity 77.8%; Pred. No. 4.1e+02;
Matches 21; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 761 TCCCGACGATCTTCTGCTCCACAC 787
Db 1 UCCCGACGATCTTCTGCTCCACAC 27

RESULT 7

US-10-708-204-5526
; Sequence 5526, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5526
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5526

Query Match 2.7%; Score 27; DB 9; Length 27;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 24; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 829 TCACCCAGGAGTGGCAAGAGAGTC 855
Db 1 UCACCCAGGAGGAGGCAAGAGAGAC 27

RESULT 8

US-10-708-204-5539
; Sequence 5539, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5539
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5539

Query Match 2.7%; Score 27; DB 9; Length 27;

```
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 24; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 828 GTCACCCAGGAGTGGCAAGAGAGT 854
Db 1 GUCACCCAGGAGGAGGCAAGAGAGU 27

RESULT 9
US-10-708-204-5537/c
; Sequence 5537, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5537
; LENGTH: 30
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5537

Query Match 2.7%; Score 27; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 978 GCTATGCCAGTCAGTGCAGCCCTC 1004
Db 30 GCTATGCCAGTCAGTGCAGCCCTC 4

RESULT 10
US-10-708-204-5530
; Sequence 5530, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5530
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-5530

Query Match 2.6%; Score 26; DB 9; Length 26;
Best Local Similarity 80.8%; Pred. No. 8.5e+02;
Matches 21; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 762 CCCGACGATCTCTCGGTCCACAC 787
Db 1 CCCGACGAUCCUCCGCGCCACAC 26

RESULT 11
US-09-067-638B-88
; Sequence 88, Application US/09067638B
; Patent No. US2002028923A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowert
; APPLICANT: Brenda F. Baker
```

```
; APPLICANT: John McNeil
; APPLICANT: Susan M. Preier
; APPLICANT: Henri M. Sasnor
; APPLICANT: Douglas G. Brooks
; APPLICANT: Cara Ohashi
; APPLICANT: Jacqueline R. Wyatt
; APPLICANT: Alexander Borchers
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Identification of Genetic
; TITLE OF INVENTION: Targets for Modulation By Oligonucleotides and
; TITLE OF INVENTION: Generation of Oligonucleotides for Gene
; TITLE OF INVENTION: Modulation
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOODCOCK WASHBURN KURTZ
; ADDRESSEE: MACKIEWICZ & NORRIS LLP
; STREET: 1 LIBERTY PLACE 46TH FLOOR
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: IBM
; OPERATING SYSTEM: PC-Windows NT
; SOFTWARE: WORD PERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,638B
; FILING DATE: 28-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/081,483
; FILING DATE: 13-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-2960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-067-638B-88

Query Match 2.5%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTGGCGTGAAAGCGAATTCCT 250
Db 1 TTCCTTGGCGTGAAAGCGAATTCCT 25

RESULT 12
US-10-116-325-88
; Sequence 88, Application US/10116325
; Publication No. US20030113739A1
; GENERAL INFORMATION:
; APPLICANT: Cowert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Identification of Genetic Targets For Modulation By Oligonucleoti
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; TITLE OF INVENTION: Generation Of Oligonucleotides For Gene Modulation
; FILE REFERENCE: ISIS5086
; CURRENT APPLICATION NUMBER: US/10/116,325
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030113739A1el Sequence
US-10-116-325-88

Query Match          2.5%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 TTCCTTGGCGTGAAGCGGAATTCCT 250
Db 1 TTCCTTGGCGTGAAGCGGAATTCCT 25

RESULT 13
US-10-234-764-14
; Sequence 14, Application US/10234764
; Publication No. US20030113769A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Lonnberg, Harri
; APPLICANT: Salo, Harri
; APPLICANT: Virta, Pasi
; TITLE OF INVENTION: Aminoxy Functionalized Oligomers
; FILE REFERENCE: ISIS5089
; CURRENT APPLICATION NUMBER: US/10/234,764
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 09/344,260
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-234-764-14

Query Match          2.5%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 TTCCTTGGCGTGAAGCGGAATTCCT 250
Db 1 TTCCTTGGCGTGAAGCGGAATTCCT 25

RESULT 14
US-10-388-263-88
; Sequence 88, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freiler, Susan M.
; APPLICANT: Sasmor, Henri M.
```

```
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-388-263-88

Query Match          2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 TTCCTTGGCGTGAAGCGGAATTCCT 250
Db 1 TTCCTTGGCGTGAAGCGGAATTCCT 25

RESULT 15
US-10-719-956-21131
; Sequence 21131, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21131
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-21131

Query Match          2.5%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 AACACTGCTGCTCCAGTCAGGAG 807
Db 1 AACACTGCTGCTCCAGTCAGGAG 25

RESULT 16
US-10-698-689-88
; Sequence 88, Application US/10698689
; Publication No. US20040186071A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowser, Lex M.
; APPLICANT: Malik, Leila
; APPLICANT: Siwkowski, Andrew
; APPLICANT: Eldrup, Anne B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 EXPRESSION
; FILE REFERENCE: ISIS-5315
; CURRENT APPLICATION NUMBER: US/10/698,689
; CURRENT FILING DATE: 2003-10-31
```

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; PRIOR APPLICATION NUMBER: PCT/US03/31166
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 10/261,382
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-698-689-88

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      226 TTCTTCGGGTGAAAGCGAATTCTT 250
Db      1   TTCTTCGGGTGAAAGCGAATTCTT 25
          |||||||||||||||||||
RESULT 17
US-10-830-475-88
; Sequence 88, Application US/10830475
; Publication No. US20040197814A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; Brenda F. Baker
; John McNeil
; Susan M. Freier
; Henri M. Sasmor
; Douglas G. Brooks
; Cara Ohashi
; Jacqueline R. Wyatt
; Alexander Borchers
; Timothy A. Vickers
; TITLE OF INVENTION: Identification of Genetic
; Targets for Modulation By Oligonucleotides and
; Generation of Oligonucleotides for Gene
; Modulation
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOODCOCK WASHBURN KURTZ
; MACKIEWICZ & NORRIS LLP
; STREET: 1 LIBERTY PLACE 46TH FLOOR
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: IBM
; OPERATING SYSTEM: PC-Windows NT
; SOFTWARE: WORD PERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/830,475
; FILING DATE: 21-Apr-2004
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,638B
; FILING DATE: 28-APR-1998
; APPLICATION NUMBER: 60/081,483
; FILING DATE: 13-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-2960
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-10-830-475-88

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      226 TTCTTCGGGTGAAAGCGAATTCTT 250
Db      1   TTCTTCGGGTGAAAGCGAATTCTT 25
          |||||||||||||||||||
RESULT 18
US-10-649-467-88
; Sequence 88, Application US/10649467
; Publication No. US20050033524A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseert
; APPLICANT: Brenda F. Baker
; APPLICANT: John McNeil
; APPLICANT: Susan M. Freier
; APPLICANT: Henri M. Sasmor
; APPLICANT: Douglas G. Brooks
; APPLICANT: Cara Ohashi
; APPLICANT: Jacqueline R. Wyatt
; APPLICANT: Alexander Borchers
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Identification of Genetic Targets for Modulation By Oligonucleotides for Gene Modulation
; FILE REFERENCE: ISIS0085-100 (ISIS2960US.C2)
; CURRENT APPLICATION NUMBER: US/10/649,467
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 09/067,636
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligomeric compound
US-10-649-467-88

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      226 TTCTTCGGGTGAAAGCGAATTCTT 250
Db      1   TTCTTCGGGTGAAAGCGAATTCTT 25
          |||||||||||||||||||
RESULT 19
US-10-809-189-44613
; Sequence 44613, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
```

; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44613

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGGTTCGTCCTCGCTCTGCGTGG 72
|||||
Db 1 ATGGTTCGTCCTCGCTCTGCGTGG 25

RESULT 20
US-10-809-189-44614
; Sequence 44614, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44614

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 CGTCTGCTCTGCGTGGTCTCT 78
|||||
Db 1 CGTCTGCTCTGCGTGGTCTCT 25

RESULT 21
US-10-809-189-44615
; Sequence 44615, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44615
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44615

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 TTGTGCCAGCCAGGACAGAACTGG 189
|||||
Db 1 TTGTGCCAGCCAGGACAGAACTGG 25

RESULT 22
US-10-809-189-44616
; Sequence 44616, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44616

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 GACTGCACAGAGTTCACTGAAACGG 219
|||||
Db 1 GACTGCACAGAGTTCACTGAAACGG 25

RESULT 23
US-10-809-189-44617
; Sequence 44617, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 44617
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44617

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      213 GAAACGGAATGCCTTCCTTGGCGTG 237
Db      1 GAAACGGAATGCCTTCCTTGGCGTG 25

RESULT 24
US-10-809-189-44618
; Sequence 44618, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44618
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44618

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      219 GAATGCCTTCCTTCGCGTGAAGCG 243
Db      1 GAATGCCTTCCTTCGCGTGAAGCG 25

RESULT 25
US-10-809-189-44619
; Sequence 44619, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44619

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      222 TGCCTTCCTTCGCGTGAAGCGAAT 246
Db      1 TGCCTTCCTTCGCGTGAAGCGAAT 25

RESULT 26
US-10-809-189-44620
; Sequence 44620, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44620
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44620

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      240 AGCGAATTCCTAGACACCTGGAACA 264
Db      1 AGCGAATTCCTAGACACCTGGAACA 25

RESULT 27
US-10-809-189-44621
; Sequence 44621, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44621

Query Match      2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Qy 243 GAATTCCTAGACACCTGGACAG 267
|||||
Db 1 GAATTCCTAGACACCTGGACAG 25

RESULT 28
US-10-809-189-44622
; Sequence 44622, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44622

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 AGAGAGACACTGCCACAGCACA 288
|||||
Db 1 AGAGAGACACTGCCACAGCACA 25

RESULT 29
US-10-809-189-44623
; Sequence 44623, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44623
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44623

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 CACTGCCACAGCAAAATACTGCG 297
|||||
Db 1 CACTGCCACAGCAAAATACTGCG 25

RESULT 30
US-10-809-189-44624
; Sequence 44624, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44624

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 TGCCACCAGCACAAATACTGCGACC 300
|||||
Db 1 TGCCACCAGCACAAATACTGCGACC 25

RESULT 31
US-10-809-189-44625
; Sequence 44625, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44625

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 CTGCCTCTGCAGTGCCTCTCTGGG 81
|||||
Db 1 CTGCCTCTGCAGTGCCTCTCTGGG 25

RESULT 32
US-10-809-189-44626
; Sequence 44626, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:

```
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44626
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```
Query Match      2.5%  Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 CCTCTGCAGTGCCTCTCTGGGGCT 84
Db 1 CCTCTGCAGTGCCTCTCTGGGGCT 25
```

```
RESULT 33
US-10-809-189-44627
; Sequence 44627, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44627
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```
Query Match      2.5%  Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 CTGCAGTGCCTCTCTCTGGGGCTGT 87
Db 1 CTGCAGTGCCTCTCTCTGGGGCTGT 25
```

```
RESULT 34
US-10-809-189-44628
; Sequence 44628, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
```

```
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44628
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```
Query Match      2.5%  Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 TTGCTGACCGCTGTCCATCCAGAAC 111
Db 1 TTGCTGACCGCTGTCCATCCAGAAC 25
```

```
RESULT 35
US-10-809-189-44629
; Sequence 44629, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44629
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44629
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Query Match      2.5%  Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CCCACTGTCATGCAGAGAAAAACAGT 138
Db 1 CCCACTGTCATGCAGAGAAAAACAGT 25
```

```
RESULT 36
US-10-809-189-44630
; Sequence 44630, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44630
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44630

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 TACCTAATAAACAGTCAGTGTGTT 162
Db 1 TACCTAATAAACAGTCAGTGTGTT 25

RESULT 37
US-10-809-189-44631
; Sequence 44631, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44631

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 AACAGTCAGTCTGTTCTTTGTGCC 171
Db 1 AACAGTCAGTCTGTTCTTTGTGCC 25

RESULT 38
US-10-809-189-44632
; Sequence 44632, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44632

; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-44632

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 162 TCTTTGTGCCAGCCAGGACAGAAAC 186
Db 1 TCTTTGTGCCAGCCAGGACAGAAAC 25

RESULT 39
US-10-956-157-22769
; Sequence 22769, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22769
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22769

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 585 AACAAAGACTGATGTTGTCTGTGTC 609
Db 1 AACAAAGACTGATGTTGTCTGTGTC 25

RESULT 40
US-10-956-157-22770
; Sequence 22770, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22770
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-22770

Query Match 2.5%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 582 ACACAAAGACTGATGTTGTCTGTG 606
Db 1 ACACAAAGACTGATGTTGTCTGTG 25

RESULT 41

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 09:46:00 ; Search time 394 Seconds

(without alignments)
2135.598 Million cell updates/sec

Title: US-10-698-689-85

Perfect score: 1004

Sequence: 1 gccctgcctggcgcccgagt.....ccagtcagtcgacgcccctc 1004

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 11560300

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

Database : Published Applications NA New:*

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3: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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11: /cgm2_6/ptodata/2/pubpna/US15_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	2.7	36	9	US-11-105-172-9
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4	25	2.5	25	8	US-11-121-849-44636
5	25	2.5	25	8	US-11-121-849-44637
6	25	2.5	25	8	US-11-121-849-44638
7	25	2.5	25	8	US-11-121-849-44639
8	25	2.5	25	8	US-11-121-849-44640
9	25	2.5	25	8	US-11-121-849-44641
10	25	2.5	25	8	US-11-121-849-44642
11	25	2.5	25	8	US-11-121-849-44643
12	25	2.5	25	8	US-11-121-849-44644
13	25	2.5	25	8	US-11-121-849-44645
14	25	2.5	25	8	US-11-121-849-44646
15	25	2.5	25	8	US-11-121-849-44647
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18	25	2.5	25	8	US-11-121-849-44650
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42	25	2.5	25	8	US-11-121-849-44674
43	25	2.5	25	8	US-11-121-849-44675
44	25	2.5	25	8	US-11-121-849-44676
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47	25	2.5	25	8	US-11-121-849-44679
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59	25	2.5	25	8	US-11-121-849-44691
60	25	2.5	25	8	US-11-121-849-44692
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65	25	2.5	25	8	US-11-121-849-44697
66	25	2.5	25	8	US-11-121-849-44698
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70	25	2.5	25	8	US-11-121-849-44702
71	25	2.5	25	8	US-11-121-849-44703
72	25	2.5	25	8	US-11-121-849-44704
73	25	2.5	25	8	US-11-121-849-44705
74	25	2.5	25	8	US-11-121-849-44706
75	25	2.5	25	8	US-11-121-849-44707
76	25	2.5	25	8	US-11-121-849-44708
77	25	2.5	25	8	US-11-121-849-44709
78	25	2.5	25	8	US-11-121-849-44710
79	25	2.5	25	8	US-11-121-849-44711
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82	25	2.5	25	8	US-11-121-849-44714
83	25	2.5	25	8	US-11-121-849-44715
84	25	2.5	25	8	US-11-121-849-44716
85	25	2.5	25	8	US-11-121-849-44717
86	25	2.5	25	8	US-11-121-849-44718
87	25	2.5	25	8	US-11-121-849-44719
88	25	2.5	25	8	US-11-121-849-44720
89	25	2.5	25	8	US-11-121-849-44721
90	25	2.5	25	8	US-11-121-849-44722
91	25	2.5	25	8	US-11-121-849-44723
92	25	2.5	25	8	US-11-121-849-44724
93	25	2.5	25	8	US-11-121-849-44725
94	25	2.5	25	8	US-11-121-849-44726
95	25	2.5	25	8	US-11-121-849-44727

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US-11-121-849-4

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96 19 1.9 19 9 US-11-101-244-1869 Sequence 1869, Ap
97 19 1.9 19 9 US-11-101-244-1870 Sequence 1870, Ap
98 19 1.9 19 9 US-11-101-244-82634 Sequence 82634, A
99 19 1.9 19 9 US-11-101-244-82635 Sequence 82635, A
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102 19 1.9 19 9 US-11-101-244-82638 Sequence 82638, A
103 19 1.9 19 9 US-11-101-244-82639 Sequence 82639, A
104 19 1.9 19 9 US-11-101-244-82640 Sequence 82640, A
105 19 1.9 19 9 US-11-101-244-82642 Sequence 82642, A
106 19 1.9 19 9 US-11-101-244-82644 Sequence 82644, A
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109 19 1.9 19 9 US-11-101-244-82648 Sequence 82648, A
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113 19 1.9 19 9 US-11-101-244-82653 Sequence 82653, A
114 19 1.9 19 9 US-11-101-244-82654 Sequence 82654, A
115 19 1.9 19 9 US-11-101-244-82655 Sequence 82655, A
116 19 1.9 19 9 US-11-101-244-82657 Sequence 82657, A
117 19 1.9 19 9 US-11-101-244-82658 Sequence 82658, A
118 19 1.9 19 9 US-11-101-244-82659 Sequence 82659, A
119 19 1.9 19 9 US-11-101-244-82660 Sequence 82660, A
120 19 1.9 19 9 US-11-101-244-82661 Sequence 82661, A
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ALIGNMENTS

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RESULT 1
US-11-105-172-9
; Sequence 9, Application US/11105172
; Publication No. US20050244370A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; TITLE OF INVENTION: Selective local activation of members of the TNF
; TITLE OF INVENTION: receptor family by systemically inactive
; TITLE OF INVENTION: non-antibody TNF ligand fusion proteins
; FILE REFERENCE: 2910-1-001
; CURRENT APPLICATION NUMBER: US/11/105,172
; CURRENT FILING DATE: 2005-04-13
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Primer 1160
US-11-105-172-9
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Query Match 2.7%; Score 27; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 42 CTCGCCATGGTTCCTCTGCTCTGCTCTGCAG 68
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Db 10 CTCGCCATGGTTCCTCTGCTCTGCTCTGCAG 36
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RESULT 2
US-11-105-172-10/c
; Sequence 10, Application US/11105172
; Publication No. US20050244370A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; TITLE OF INVENTION: Selective local activation of members of the TNF
; TITLE OF INVENTION: receptor family by systemically inactive
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; TITLE OF INVENTION: non-antibody TNF ligand fusion proteins
; FILE REFERENCE: 2910-1-001
; CURRENT APPLICATION NUMBER: US/11/105,172
; CURRENT FILING DATE: 2005-04-13
; PRIOR FILING DATE: DE 102 47 755.8
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Primer 1161
US-11-105-172-10
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Query Match 2.7%; Score 26.8; DB 9; Length 33;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 600 GTCTGTGTCCTCCAGGATCGCTGAGAGCC 629
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Db 33 GTCTGTGTCCTCCAGGATCGCTGAGATCC 4
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RESULT 3
US-11-121-849-44635
; Sequence 44635, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44635
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44635
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Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 375 CACTGTACGAGTGAGCGCTGTGAGA 399
| | | | | | | | | | | | | | | | | |
Db 1 CACTGTACGAGTGAGCGCTGTGAGA 25
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RESULT 4
US-11-121-849-44636
; Sequence 44636, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44636
; LENGTH: 25
; TYPE: DNA
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US-11-121-849-44639
; ORGANISM: Homo sapien
; Sequence 44639, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44637
; Sequence 44637, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44637

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 399 GCCTGTGAGAGCTGTGCTCGACC 414
Db 1 GCCTGTGAGAGCTGTGCTCGACC 25

RESULT 5
US-11-121-849-44637
; Sequence 44637, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44638
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44638

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 420 TGCTGCCCCGGCTTTGGGTCAAGC 444
Db 1 TGCTGCCCCGGCTTTGGGTCAAGC 25

RESULT 7

US-11-121-849-44639
; Sequence 44639, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44639
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44639

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 439 TCAAGCAGATTGCTACAGGGGTTTC 463
Db 1 TCAAGCAGATTGCTACAGGGGTTTC 25

RESULT 8
US-11-121-849-44640
; Sequence 44640, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44640
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44640

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 461 TTCTGATACCATCTCGAGCCCTGC 485
Db 1 TTCTGATACCATCTCGAGCCCTGC 25

RESULT 9
US-11-121-849-44641
; Sequence 44641, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44641
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44641

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 484 GCCAGTCGGTCTCTTCCCAATCT 508
|||||
Db 1 GCCAGTCGGTCTCTTCCCAATCT 25

RESULT 10

US-11-121-849-44642
; Sequence 44642, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44642
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44642

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 498 TTCTCCAATGTGTCATCTGCTTCG 522
|||||
Db 1 TTCTCCAATGTGTCATCTGCTTCG 25

RESULT 11

US-11-121-849-44643
; Sequence 44643, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44643

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 ATGTGTCATCTGCTTTTCGAAAAATG 529
|||||

Db 1 ATGTGTCATCTGCTTTTCGAAAAATG 25

RESULT 12

US-11-121-849-44644
; Sequence 44644, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44644

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 519 TTCGAAAAATGTCACCTTCGACAA 543
|||||
Db 1 TTCGAAAAATGTCACCTTCGACAA 25

RESULT 13

US-11-121-849-44645
; Sequence 44645, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44645

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 579 GGCACAAACAAAGACTGATGTGTCT 603
|||||
Db 1 GGCACAAACAAAGACTGATGTGTCT 25

RESULT 14

US-11-121-849-44646
; Sequence 44646, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44646
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44646

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 589 AGACTGATGTTCTCTGTGTCGCCCA 613
|||||
Db 1 AGACTGATGTTCTCTGTGTCGCCCA 25

RESULT 15

US-11-121-849-44647
; Sequence 44647, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44647
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44647

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 590 GACTGATGTTCTCTGTGTCGCCAG 614
|||||
Db 1 GACTGATGTTCTCTGTGTCGCCAG 25

RESULT 16

US-11-121-849-44648
; Sequence 44648, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44648

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 GCTGAGACCCCTGGTGGTATCCCC 644
|||||
Db 1 GCTGAGACCCCTGGTGGTATCCCC 25

RESULT 17

US-11-121-849-44649
; Sequence 44649, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44649

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 CCCTGGTGGTATCCCATCATCTT 652
|||||
Db 1 CCCTGGTGGTATCCCATCATCTT 25

RESULT 18

US-11-121-849-44650
; Sequence 44650, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 44650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-44650

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 658 TCCTGTTTGCATCCTCTTGTGCT 682
|||||
Db 1 TCCTGTTTGCATCCTCTTGTGCT 25

RESULT 19

US-11-121-849-46828
; Sequence 46828, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma

```

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46828

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred.No.3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      810 TTACATGGATGCCCAACCGGTCACCC 834
Db      1 TTACATGGATGCCCAACCGGTCACCC 25

RESULT 20
US-11-121-849-46829
; Sequence 46829, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46829
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46829

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred.No.3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      811 TACATGGATGCCCAACCGGTCACCCCA 835
Db      1 TACATGGATGCCCAACCGGTCACCCCA 25

RESULT 21
US-11-121-849-46830
; Sequence 46830, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46830
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46830

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```
; Sequence 46833, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46833
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46833

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      895 CAGGAGTGTGGCCAGCGGCAAC 919
      |||||||
Db      1 CAGGAGTGTGGCCAGCGGCAAC 25

RESULT 25
US-11-121-849-46834
; Sequence 46834, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46834
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46834

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      914 GCAACAGCGCAGTTGGCCAGAGGC 938
      |||||||
Db      1 GCAACAGCGCAGTTGGCCAGAGGC 25

RESULT 26
US-11-121-849-46835
; Sequence 46835, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 46835
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46835

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      915 CAAACAGCGCAGTTGGCCAGAGGCC 939
      |||||||
Db      1 CAAACAGCGCAGTTGGCCAGAGGCC 25

RESULT 27
US-11-121-849-46836
; Sequence 46836, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46836
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46836

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      916 AAACAGCGCAGTTGGCCAGAGGCCT 940
      |||||||
Db      1 AAACAGCGCAGTTGGCCAGAGGCCT 25

RESULT 28
US-11-121-849-46837
; Sequence 46837, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-46837

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      920 AGGCAGTTGGCCAGAGGCCTGGTG 944
      |||||||
Db      1 AGGCAGTTGGCCAGAGGCCTGGTG 25
```

```

; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141447
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141447

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      823 AACCGGTCACCCAGGAGGATGGCAA 847
      |||||
Db       1 AACCGGTCACCCAGGAGGATGGCAA 25

RESULT 32
US-11-121-849-141448
; Sequence 141448, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedments
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141448
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141448

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      824 ACCGGTCACCCAGGAGGATGGCAA 848
      |||||
Db       1 ACCGGTCACCCAGGAGGATGGCAA 25

RESULT 33
US-11-121-849-141449
; Sequence 141449, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedments
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141449
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141449

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 826 CGGTACCCAGGAGTGCAGAGA 850
Db 1 CGGTACCCAGGAGTGCAGAGA 25

RESULT 34

US-11-121-849-141450
; Sequence 141450, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141450

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 828 CTCACCCAGGAGTGCAGAGA 852
Db 1 CTCACCCAGGAGTGCAGAGA 25

RESULT 35

US-11-121-849-141451
; Sequence 141451, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141451

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GATGCAAGAGATCGCATCTCAG 864
Db 1 GATGCAAGAGATCGCATCTCAG 25

RESULT 36

US-11-121-849-141452
; Sequence 141452, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141452
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141452

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 843 GGCAGAGAGTGCATCTCAGTC 867
Db 1 GGCAGAGAGTGCATCTCAGTC 25

RESULT 37

US-11-121-849-141453
; Sequence 141453, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141453
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141453

Query Match 2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 AAGAGTGCATCTCAGTCAGGA 871
Db 1 AAGAGTGCATCTCAGTCAGGA 25

RESULT 38

US-11-121-849-141454
; Sequence 141454, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141454
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141454

```
Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 849 GAGAGTCGATCTCTCAGTCGAGGAGA 873
|||||
Db 1 GAGAGTCGATCTCTCAGTCGAGGAGA 25

RESULT 39
US-11-121-849-141455
; Sequence 141455, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141455

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 851 GAGTCGCATCTCTCAGTCGAGGAGA 875
|||||
Db 1 GAGTCGCATCTCTCAGTCGAGGAGA 25

RESULT 40
US-11-121-849-141456
; Sequence 141456, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 141456
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-141456

Query Match      2.5%; Score 25; DB 8; Length 25;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 873 AGACAGTGAGCTGCACCCACCCAG 897
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RESULT 41
US-11-121-849-405290
; Sequence 405290, Application US/11121849
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 405290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-405290

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGACAGTGAGCTGCACCCACCCAG 25

RESULT 42
US-11-121-849-405291/c
; Sequence 405291, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 405291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-405291

Query Match      2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 975 GGAGCTATGCCAGTCAGTCGCCAGC 999
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Db 25 GGAGCTATGCCAGTCAGTCGCCAGC 1

RESULT 43
US-11-136-527-244207
; Sequence 244207, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AMI101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 244207
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-244207

Query Match          2.5%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
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QY  847 AAGAGAGTCGCATCTCAGTGCAGGA 871
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RESULT 44
US-10-924-074-18
; Sequence 18, Application US/10924074
; Publication No. US20050272050A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Bernstein, Jeanne
; APPLICANT: Eshel, Dani
; APPLICANT: Toporik, Amir
; APPLICANT: Chen, Aviva
; TITLE OF INVENTION: CD40 Splice Variants, Compositions for Making and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 28800-501 CIP
; CURRENT APPLICATION NUMBER: US/10/924,074
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: PCT/IB03/0665
; PRIOR FILING DATE: 2003-02-23
; PRIOR APPLICATION NUMBER: 60/358,877
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-924-074-18

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 45
US-10-310-914A-402300
; Sequence 402300, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 402300
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-402300

Query Match          2.4%; Score 24; DB 7; Length 24;
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Best Local Similarity 95.8%; Pred. No. 7.3e+02;
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Db    1 GGGGUGCAGGCAGAAAGCGGGGAGC 24

Search completed: February 5, 2006, 12:44:19
Job time : 395 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 08:42:01 ; Search time 5162 Seconds
(without alignments)
11055.952 Million cell updates/sec

Title: US-10-698-689-85
Perfect score: 1004
Sequence: 1 gctcgcctcgggccagcgt.....ccagtcagtcgacgccctc 1004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

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3: gb_env.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	3.3	40	6	BD182308
2	33	3.3	40	6	AX327715
3	28	2.8	28	6	AR090351
4	28	2.8	28	6	AR090352
5	28	2.8	28	6	AR197386
6	28	2.8	28	6	AR197387
7	28	2.8	28	6	AR259540
8	28	2.8	28	6	AR259541
9	27	2.7	36	6	CQ803276
10	26.8	2.7	33	6	CQ803277
11	25	2.5	25	6	AR138078
12	25	2.5	25	6	BD226629
13	25	2.5	25	6	BD250534
14	25	2.5	25	6	AR343051
15	25	2.5	25	6	AR611142
16	25	2.5	33	6	AX746460
17	25	2.5	33	6	AX763806
18	25	2.5	50	6	AX093091

C	19	24.6	2.5	35	6	CQ970331	Sequence
C	20	24.6	2.5	35	6	CQ970340	Sequence
	21	24	2.4	24	6	CQ790416	Sequence
	22	24	2.4	24	6	AX027448	Sequence
	23	24	2.4	24	6	AX406771	Sequence
	24	24	2.4	24	6	AX746094	Sequence
	25	24	2.4	24	6	AX770445	Sequence
	26	24	2.4	24	6	AX823741	Sequence
	27	24	2.4	32	6	AR004297	Sequence
	28	24	2.4	32	6	AR004299	Sequence
	29	24	2.4	32	6	AR032329	Sequence
	30	24	2.4	32	6	AR032331	Sequence
	31	24	2.4	32	6	AR095273	Sequence
	32	24	2.4	32	6	AR178093	Sequence
	33	24	2.4	32	6	I69320	Sequence
	34	24	2.4	32	6	AR659104	Sequence
	35	24	2.4	34	6	AR004298	Sequence
	36	24	2.4	34	6	AR032330	Sequence
	37	24	2.4	34	6	AR095274	Sequence
	38	24	2.4	34	6	AR178094	Sequence
	39	24	2.4	34	6	I69321	Sequence
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	44	23	2.3	23	6	BD226628	Antisense
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	49	23	2.3	23	6	AR343050	Sequence
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	52	22.2	2.2	23	6	BD211595	Canine an
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	57	22.2	2.2	50	6	CQ004366	Sequence
	58	22.2	2.2	50	6	CQ004370	Sequence
	59	22	2.2	50	6	AX823744	Sequence
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	61	21.6	2.2	50	6	CQ004406	Sequence
	62	21.4	2.1	47	6	BD232083	Complex f
	63	21.2	2.1	32	6	AX746461	Sequence
	64	21.2	2.1	32	6	AX763807	Sequence
	65	21.2	2.1	39	6	AX403813	Sequence
	66	21	2.1	31	6	BD002823	Gene comp
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	69	21	2.1	49	6	CQ970233	Sequence
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	71	20.6	2.1	21	6	AX095599	Sequence
	72	20.6	2.1	42	6	BD209058	Enzymatic
	73	20.6	2.1	47	6	AR289089	Sequence
	74	20.6	2.1	48	8	HS3B3VB19	X84265 H.sapiens m
	75	20.6	2.1	50	6	CQ006589	Sequence
	76	20.4	2.0	42	6	BD203540	Method an
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	78	20.2	2.0	21	6	BD211594	Canine an
	79	20.2	2.0	21	6	AR241572	Sequence
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	82	20.2	2.0	46	6	AR399747	Sequence
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	86	20	2.0	20	6	CQ790417	Sequence
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	88	20	2.0	20	6	AX406772	Sequence
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c 94 20 2.0 47 6 AR291860
c 95 20 2.0 50 9 MWVIMV21
c 96 19.8 2.0 24 6 AR652475
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102 19.6 2.0 29 6 BD273645
103 19.6 2.0 29 6 AR322271
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c 105 19.6 2.0 35 6 BD188203
106 19.6 2.0 42 6 BD201771
107 19.6 2.0 42 6 BD203472
c 108 19.6 2.0 50 6 BD273138
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111 19.4 1.9 21 6 AR580026
c 112 19.4 1.9 21 6 AR580027
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114 19.4 1.9 50 6 AR024001
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116 19.4 1.9 50 6 BD068875
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ALIGNMENTS

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BD182308
LOCUS BD182308 40 bp DNA linear PAT 15-MAY-2003
DEFINITION Anti CD40 monoclonal antibody.
ACCESSION BD182308
VERSION BD182308.1 GI:30793226
KEYWORDS WO 02088186-A/1.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mikayama,T., Yoshida,H., Force,W.R., Chen,X. and Takahashi,N.
TITLE Anti CD40 monoclonal antibody
JOURNAL KIRIN BREWERY CO LTD,TOSHIFUMI MIKAYAMA,HITOSHI YOSHIDA, WALKER R
COMMENT OS Artificial Sequence
PN WO 02088186-A/1
PD 07-NOV-2002
PF 26-APR-2002 WO 2002JP004292
PR 27-APR-2001 WO PCTUS0113672.11-MAY-2001 JP 01P 142482 PR
05-OCT-2001 JP 01P 310535.26-OCT-2001 US 10/040244 PI
TOSHIFUMI MIKAYAMA,HITOSHI YOSHIDA,WALKER
R FORCE,XINGJIE CHEN,NOBUAKI TAKAHASHI
PI NOBUAKI TAKAHASHI
PC C07K16/28,C12N15/13,C12N5/10,C12P21/08,A61K39/395,A61P35/00,
PC A61P37/04,
PC A61P37/06,A61P37/08,A61P7/00
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CC Location/Qualifiers
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AX327715
LOCUS AX327715 40 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0183755.
ACCESSION AX327715
VERSION AX327715.1 GI:18098026
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mikayama,T., Takahashi,N., Chen,X. and Schoenberger,S.P.
TITLE Human anti-cd40 antibodies and methods of making and using same
JOURNAL Patent: WO 0183755-A 1 08-NOV-2001;
Geminii Science, Inc. (US)
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/note="Primer"
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ORIGIN

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RESULT 3
AR090351
LOCUS AR090351 28 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 471 from patent US 5994076.
ACCESSION AR090351
VERSION AR090351.1 GI:10017106
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 471 30-NOV-1999;
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DEFINITION Sequence 472 from patent US 5994076.
ACCESSION AR090352
VERSION AR090352.1 GI:10017107
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 472 30-NOV-1999;
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Best Local Similarity 100.0%; Pred. No. 3.4e+04;
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Db 28 CAGGCACAAACAAGACTGATGTTGCTG 1

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LOCUS AR259540 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 471 from patent US 6489455.
ACCESSION AR259540
VERSION AR259540.1 GI:27310051
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 471 03-DEC-2002;
FEATURES Clontech Laboratories, Inc.; Palo Alto, CA
Location/Qualifiers
source 1..28
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/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 3.4e+04;
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DEFINITION Sequence 472 from patent US 6489455.
ACCESSION AR259541
VERSION AR259541.1 GI:27310052
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 472 03-DEC-2002;
FEATURES Clontech Laboratories, Inc.; Palo Alto, CA
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Query Match 2.8%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 577 CAGGCACAAACAAGACTGATGTTGCTG 604
Db 28 CAGGCACAAACAAGACTGATGTTGCTG 1

RESULT 9
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DEFINITION Sequence 472 from patent US 5994076.
ACCESSION AR090352
VERSION AR090352.1 GI:10017107
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 472 30-NOV-1999;
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Query Match 2.8%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR197386 28 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 471 from patent US 6352829.
ACCESSION AR197386
VERSION AR197386.1 GI:20247235
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 471 05-MAR-2002;
FEATURES Location/Qualifiers
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LOCUS AR197387 28 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 472 from patent US 6352829.
ACCESSION AR197387
VERSION AR197387.1 GI:20247236
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Johhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 472 05-MAR-2002;
FEATURES Location/Qualifiers
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LOCUS CQ803276 36 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 9 from Patent WO2004035794.
ACCESSION CQ803276
VERSION CQ803276.1 GI:47110174
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Pfizenmaier, K. and Wajant, H.
AUTHORS Selective, local activation of members of the tnfr ligand family of
TITLE systemically inactive non-antibody tnfr ligand fusion proteins
JOURNAL Patent: WO 2004035794-A 9 29-APR-2004;
Pfizenmaier, Klaus (DE); Wajant, Harald (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der k nstlichen Sequenz: Primer 1160"

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Best Local Similarity 100.0%; Pred. No. 6.4e+04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 CTCGCCATGGTTCGTCTGCCTCTGCAG 68
|||||
Db 10 CTCGCCATGGTTCGTCTGCCTCTGCAG 36
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RESULT 10
CQ803277/c
LOCUS CQ803277 33 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 10 from Patent WO2004035794.
ACCESSION CQ803277
VERSION CQ803277.1 GI:47110175
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Pfizenmaier, K. and Wajant, H.
AUTHORS Selective, local activation of members of the tnfr ligand family of
TITLE systemically inactive non-antibody tnfr ligand fusion proteins
JOURNAL Patent: WO 2004035794-A 10 29-APR-2004;
Pfizenmaier, Klaus (DE); Wajant, Harald (DE)
FEATURES Location/Qualifiers
source 1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der k nstlichen Sequenz: Primer 1161"

ORIGIN
Query Match 2.7%; Score 26.8; DB 6; Length 33;
Best Local Similarity 93.3%; Pred. No. 7.3e+04;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 600 GTCTGTGTCCTCCAGGATCGCTGAGGCC 629
|||||
Db 33 GTCTGTGTCCTCCAGGATCGCTGAGTCC 4
|||||

RESULT 11
ARI38078
LOCUS ARI38078 25 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 88 from patent US 6197584.
ACCESSION ARI38078
VERSION ARI38078.1 GI:14479587
KEYWORDS Unknown.
SOURCE Unknown.

Unclassified.
1 (bases 1 to 25)
Bennett, C. Frank, and Cowser, L. M.
Antisense modulation of CD40 expression
Patent: US 6197584-A 88 06-MAR-2001;
JOURNAL Location/Qualifiers
FEATURES source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTCGGTGAAGCGAATTCCT 250
|||||
Db 1 TTCCTTCGGTGAAGCGAATTCCT 25
|||||

RESULT 12
BD226629
LOCUS BD226629 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of CD40 expression.
ACCESSION BD226629
VERSION BD226629.1 GI:33036399
KEYWORDS JP 2002513593-A/88.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Bennett, C. F. and Cowser, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: JP 2002513593-A 88 14-MAY-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2002513593-A/88
PD 14-MAY-2002
PF 22-APR-1999 JP 2000547271
PR 01-MAY-1998 US 09/071433
PI C FRANK BENNETT, LEX M COWSERT
PC C12N15/09, A61K9/10, A61K45/00, A61K48/00, A61P1/06, PC
A61P17/06,
PC A61P29/00, A61P35/00, A61P37/02, A61P37/06, A61P43/00, C12P19/34,
C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of CD40 expression
FH Key Location/Qualifiers
FT source 1..22
/organism="Unidentified".
FEATURES Location/Qualifiers
source 1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TTCCTTCGGTGAAGCGAATTCCT 250
|||||
Db 1 TTCCTTCGGTGAAGCGAATTCCT 25
|||||

RESULT 13
BD250534
LOCUS BD250534 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of genetic targets for modulation by
oligonucleotides and generation of oligonucleotides for gene

modulation.
ACCESSION BD250534
VERSION BD250534.1 GI:33060304
SOURCE JP 2002511276-A/88.
KEYWORDS synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M., Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation
JOURNAL Patent: JP 2002511276-A 88 16-APR-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002511276-A/88
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASNOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
C12N15/00
CC PCR Probe Location/Qualifiers
FH Key 1..25
FT source /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
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DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 14
AR343051
LOCUS AR343051 25 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6576752.
ACCESSION AR343051
VERSION AR343051.1 GI:33738379
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminoxy functionalized oligomers
JOURNAL Patent: US 6576752-A 14 10-JUN-2003;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
|||||
DB 1 TTCCTTGGGTGAAGCGAATTCCT 250
modulation.
ACCESSION BD250534
VERSION BD250534.1 GI:33060304
SOURCE JP 2002511276-A/88.
KEYWORDS synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M., Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation
JOURNAL Patent: JP 2002511276-A 88 16-APR-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002511276-A/88
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASNOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
C12N15/00
CC PCR Probe Location/Qualifiers
FH Key 1..25
FT source /organism='Artificial Sequence'.
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source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
|||||
DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 14
AR343051
LOCUS AR343051 25 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6576752.
ACCESSION AR343051
VERSION AR343051.1 GI:33738379
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminoxy functionalized oligomers
JOURNAL Patent: US 6576752-A 14 10-JUN-2003;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
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DB 1 TTCCTTGGGTGAAGCGAATTCCT 250

|||||
DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 15
AR611142
LOCUS AR611142 25 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 14 from patent US 6825331.
ACCESSION AR611142
VERSION AR611142.1 GI:56666771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
TITLE Aminoxy functionalized oligomers, oligomer arrays and methods of using them
JOURNAL Patent: US 6825331-A 14 30-NOV-2004;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 226 TTCCTTGGGTGAAGCGAATTCCT 250
|||||
DB 1 TTCCTTGGGTGAAGCGAATTCCT 25
RESULT 16
AX746460
LOCUS AX746460 33 bp DNA linear PAT 20-JUN-2003
DEFINITION Sequence 9 from Patent EP1308167.
ACCESSION AX746460
VERSION AX746460.1 GI:32130727
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Pickl,W.
TITLE Antigen presenting vesicles
JOURNAL Patent: EP 1308167-A 9 07-MAY-2003;
Pickl, Winfried, Ao. Univ. Prof. Dr. (AT)
FEATURES
source Location/Qualifiers
1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide sequence (forward) used for making a molecule section coding for a CD40 ectodomain"
ORIGIN
Query Match 2.5%; Score 25; DB 6; Length 33;
Best Local Similarity 84.8%; Pred. No. 2.2e+05;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 95 CGCTGTCCATCCAGAACCCACTGCGATGCGAG 127
|||||
DB 1 CGCGGGGATCCCGAACCCACTGCGATGCGAG 33
RESULT 17
AX763806
LOCUS AX763806 33 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 9 from Patent WO03039594.
ACCESSION AX763806

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JOURNAL Patent: WO 2004046720-A 2 03-JUN-2004;
FEATURES Alligator Bioscience AB (SE)
source Location/Qualifiers
1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CD40 cytoplasmic and transmembrane domain oligonucleotide 2"

ORIGIN
Query Match 2.5%; Score 24.6; DB 6; Length 35;
Best Local Similarity 87.1%; Pred.No. 2.9e+05;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 859 TCTCAGTCGAGGACAGACGTGGCGTGCAC 889
Db 35 TCTCAGTCGAGGACAGACGTGGATCGACGC 5

RESULT 20
CQ970340/c
LOCUS CQ970340 35 bp DNA linear PAT 20-DEC-2004
DEFINITION Sequence 11 from Patent WO2004046720.
ACCESSION CQ970340
VERSION CQ970340.1 GI:56744111
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ellmark,P., Furebring,C., Ohlin,M. and Borrebaeck,C.
TITLE Methods for identifying members of specific binding pairs
JOURNAL Patent: WO 2004046720-A 11 03-JUN-2004;
Alligator Bioscience AB (SE)
FEATURES source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' CD40 (Sall) oligonucleotide"

ORIGIN
Query Match 2.5%; Score 24.6; DB 6; Length 35;
Best Local Similarity 87.1%; Pred.No. 2.9e+05;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 859 TCTCAGTCGAGGACAGACGTGGCGTGCAC 889
Db 35 TCTCAGTCGAGGACAGACGTGGATCGACGC 5

RESULT 21
CQ790416
LOCUS CQ790416 24 bp DNA linear PAT 29-MAR-2004
DEFINITION Sequence 37 from Patent WO2004022749.
ACCESSION CQ790416
VERSION CQ790416.1 GI:45823458
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hecker,M. and Wagner,A.H.
TITLE Decoy-oligonucleotide-inhibition of cd40-expression
JOURNAL Patent: WO 2004022749-A 37 18-MAR-2004;
Avontec GmbH (DE)
FEATURES source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
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Query Match      2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225
Db 1 CAGAGTTCACCTGAAACGGAATGCC 24

RESULT 22
AX027448
LOCUS AX027448 24 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 1 from Patent WO039294.
ACCESSION AX027448
VERSION AX027448.1 GI:10188414
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Bravery, C., Thompson, S. and Rushworth, S.
TITLE Porcine cells incapable of expressing cd40 antigen, for
JOURNAL xenotransplantation
Patent: WO 0039294-A 1 06-JUL-2000;
NOVARTIS ERFIN VERNALT GMBH (AT); NOVARTIS AG (CH); BRAVERY
CHRISTOPHER (GB); THOMPSON SIMON (GB); RUSHWORTH STUART (GB)
FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer A"

ORIGIN
Query Match      2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 TCGGCTTCTTCTCCAATGTGTCAT 513
Db 1 TCGGCTTCTTCTCCAATGTGTCAT 24

RESULT 23
AX406771
LOCUS AX406771 24 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 27 from Patent WO0229044.
ACCESSION AX406771
VERSION AX406771.1 GI:21439696
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Hecker, M. and Wagner, A.H.
TITLE Modulation of the transcription of pro-inflammatory gene products
JOURNAL Patent: WO 0229044-A 27 11-APR-2002;
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

ORIGIN
Query Match      2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225
Db 1 CAGAGTTCACCTGAAACGGAATGCC 24
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RESULT 24
AX746094
LOCUS AX746094 24 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 44 from Patent WO03031459.
ACCESSION AX746094
VERSION AX746094.1 GI:30724744
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Hecker, M. and Wagner, A.H.
TITLE Modulation of the expression of genes dependent on stat-1
JOURNAL Patent: WO 03031459-A 44 17-APR-2003;
Avontec GmbH (DE)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN
Query Match      2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225
Db 1 CAGAGTTCACCTGAAACGGAATGCC 24

RESULT 25
AX770445
LOCUS AX770445 24 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 44 from Patent WO03030944.
ACCESSION AX770445
VERSION AX770445.1 GI:32437846
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Hecker, M. and Wagner, A.H.
TITLE Inhibition of stat-1
JOURNAL Patent: WO 03030944-A 44 17-APR-2003;
Avontec GmbH (DE)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN
Query Match      2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225
Db 1 CAGAGTTCACCTGAAACGGAATGCC 24

RESULT 26
AX823741
LOCUS AX823741 24 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 18 from Patent WO03070768.
ACCESSION AX823741
VERSION AX823741.1 GI:39750074
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Bernstein,J., Mintz,L. and Eshel,D.
TITLE Cd40 splice variants, compositions for making and methods of using
the same
JOURNAL Patent: WO 03070768-A 18 28-AUG-2003;
COMPUGEN Ltd. (IL)
FEATURES Location/Qualifiers
source
1. .24
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 373 GGCACGTGTACGAGTGAGGCGCTGTG 396
|||||
Db 1 GGCACGTGTACGAGTGAGGCGCTGTG 24
RESULT 27
LOCUS AR004297 32 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 5 from patent US 5747034.
ACCESSION AR004297
VERSION AR004297.1 GI:3965176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods and materials for the induction of T cell anergy
JOURNAL Patent: US 5747034-A 5 05-MAY-1998;
FEATURES Location/Qualifiers
source
1. .32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTTCG 55
|||||
Db 9 CTGGTCTCACCTCGCCCATGGTTTCG 32
RESULT 28
LOCUS AR004299 32 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 7 from patent US 5747034.
ACCESSION AR004299
VERSION AR004299.1 GI:3965178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods and materials for the induction of T cell anergy
JOURNAL Patent: US 5747034-A 7 05-MAY-1998;
FEATURES Location/Qualifiers
source
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/organism="unknown"

ORIGIN
/mol_type="unassigned DNA"
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTTCG 55
|||||
Db 9 CTGGTCTCACCTCGCCCATGGTTTCG 32
RESULT 29
LOCUS AR032329 32 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5869050.
ACCESSION AR032329
VERSION AR032329.1 GI:5947934
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods of blocking T-cell activation using anti-B7 monoclonal
antibodies
JOURNAL Patent: US 5869050-A 5 09-FEB-1999;
FEATURES Location/Qualifiers
source
1. .32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTTCG 55
|||||
Db 9 CTGGTCTCACCTCGCCCATGGTTTCG 32
RESULT 30
LOCUS AR032331 32 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5869050.
ACCESSION AR032331
VERSION AR032331.1 GI:5947936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods of blocking T-cell activation using anti-B7 monoclonal
antibodies
JOURNAL Patent: US 5869050-A 7 09-FEB-1999;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTTCG 55
|||||
Db 9 CTGGTCTCACCTCGCCCATGGTTTCG 32
RESULT 31
LOCUS AR032331 32 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5869050.
ACCESSION AR032331
VERSION AR032331.1 GI:5947936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS de Boer,M. and Conroy,L.B.
TITLE Methods of blocking T-cell activation using anti-B7 monoclonal
antibodies
JOURNAL Patent: US 5869050-A 7 09-FEB-1999;
FEATURES Location/Qualifiers
source
1. .32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 CTGGTCTCACCTCGCCCATGGTTTCG 55
|||||
Db 9 CTGGTCTCACCTCGCCCATGGTTTCG 32
RESULT 31

AR095273
LOCUS AR095273 32 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 5 from patent US 6004552.
ACCESSION AR095273
VERSION AR095273.1 GI:10022998
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 32)
de Boer, M. and Conroy, L.B.
TITLE Methods of blocking B cell proliferation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6004552-A 5 21-DEC-1999;
FEATURES Location/Qualifiers
1..32
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 32
LOCUS AR178093 32 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 5 from patent US 6315998.
ACCESSION AR178093
VERSION AR178093.1 GI:17920986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 32)
de Boer, M. and Conroy, L.B.
TITLE Methods of blocking B-cell activation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6315998-A 5 13-NOV-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 33
LOCUS I69320 32 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 5 from patent US 5677165.
ACCESSION I69320
VERSION I69320.1 GI:2831442
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 32)
de Boer, M. and Conroy, L.B.
TITLE Anti-CD40 monoclonal antibodies capable of blocking B-cell activation

JOURNAL Patent: US 5677165-A 5 14-OCT-1997;
FEATURES Location/Qualifiers
1..32
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 34
LOCUS AR659104 32 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 5 from patent US 6899879.
ACCESSION AR659104
VERSION AR659104.1 GI:67595032
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 32)
de Boer, M. and Conroy, L.B.
TITLE Method for treating an IGE-mediated disease in a patient using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6899879-A 5 31-MAY-2005;
FEATURES Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 35
LOCUS AR004298 34 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 6 from patent US 5747034.
ACCESSION AR004298
VERSION AR004298.1 GI:3965177
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 34)
de Boer, M. and Conroy, L.B.
TITLE Methods and materials for the induction of T cell anergy
JOURNAL Patent: US 5747034-A 6 05-MAY-1998;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCCAGGAGTGTGG 905
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Db 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 36
AR032330/c
LOCUS AR032330 34 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5869050.
ACCESSION AR032330
VERSION AR032330.1 GI:5947935
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Methods of blocking T-cell activation using anti-B7 monoclonal antibodies
JOURNAL Patent: US 5869050-A 6 09-FEB-1999;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
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ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 37
AR095274/c
LOCUS AR095274 34 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 6004552.
ACCESSION AR095274
VERSION AR095274.1 GI:10023000
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Methods of blocking B cell proliferation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6004552-A 6 21-DEC-1999;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 38
AR178094/c
LOCUS AR178094 34 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 6 from patent US 6315998.
ACCESSION AR178094
VERSION AR178094.1 GI:17920987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Method for treating an IgE-mediated disease in a patient using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6315998-A 6 31-MAY-2005;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;

REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Methods of blocking B-cell activation using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6315998-A 6 13-NOV-2001;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 39
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LOCUS I69321 34 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 6 from patent US 5677165.
ACCESSION I69321
VERSION I69321.1 GI:2831443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Anti-CD40 monoclonal antibodies capable of blocking B-cell activation
JOURNAL Patent: US 5677165-A 6 14-OCT-1997;
FEATURES Location/Qualifiers
source 1. .34
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.4%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.2e+05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCCAGGAGTGTGG 905
|||||
Db 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 40
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LOCUS AR659105 34 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 6 from patent US 6899879.
ACCESSION AR659105
VERSION AR659105.1 GI:67595033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS de Boer, M. and Conroy, L.B.
TITLE Method for treating an IgE-mediated disease in a patient using anti-CD40 monoclonal antibodies
JOURNAL Patent: US 6899879-A 6 31-MAY-2005;
FEATURES Location/Qualifiers
source 1. .34
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/mol_type="genomic DNA"

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GCGTCGACCCACCCAGGAGTGG 905
Db 34 GCGTCGACCCACCCAGGAGTGG 11

RESULT 41
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LOCUS ARI38076 23 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 86 from patent US 6197584.
ACCESSION ARI38076
VERSION ARI38076.1 GI:14479585
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett, C. Frank. and Cowser, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 86 06-MAR-2001;
FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAACGGAATGC 224
Db 1 CAGAGTTCACTGAACGGAATGC 23

RESULT 42
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LOCUS ARI38077 23 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 87 from patent US 6197584.
ACCESSION ARI38077
VERSION ARI38077.1 GI:14479586
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett, C. Frank. and Cowser, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 87 06-MAR-2001;
FEATURES
source
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GAACAGAGACACACTGCCACC 282
Db 23 GAACAGAGACACACTGCCACC 1

RESULT 43
BD226627
LOCUS BD226627 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of CD40 expression.
ACCESSION BD226627
VERSION BD226627.1 GI:33036397
KEYWORDS JP 2002513593-A/86.
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SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett, C. F. and Cowser, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: JP 2002513593-A 86 14-MAY-2002;
COMMENT
OS Unidentified
PN JP 2002513593-A/86
PD 14-MAY-2002
PF 22-APR-1999 JP 2000547271
PR 01-MAY-1998 US 09/071433
PI C FRANK BENNETT, LEX M COWSERT
PC C12N15/09, A61K9/10, A61K45/00, A61K48/00, A61P1/00, A61P11/06, PC
A61P17/06,
PC A61P29/00, A61P35/00, A61P37/02, A61P37/06, A61P43/00, C12P19/34,
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of CD40 expression
FH Key Location/Qualifiers
FT source 1..23
FT Location/Qualifiers
1..23
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ORIGIN
Query Match 2.3%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAACGGAATGC 224
Db 1 CAGAGTTCACTGAACGGAATGC 23

RESULT 44
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LOCUS BD226628 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of CD40 expression.
ACCESSION BD226628
VERSION BD226628.1 GI:33036398
KEYWORDS JP 2002513593-A/87.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett, C. F. and Cowser, L. M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: JP 2002513593-A 87 14-MAY-2002;
COMMENT
OS Unidentified
PN JP 2002513593-A/87
PD 14-MAY-2002
PF 22-APR-1999 JP 2000547271
PR 01-MAY-1998 US 09/071433
PI C FRANK BENNETT, LEX M COWSERT
PC C12N15/09, A61K9/10, A61K45/00, A61K48/00, A61P1/00, A61P11/06, PC
A61P17/06,
PC A61P29/00, A61P35/00, A61P37/02, A61P37/06, A61P43/00, C12P19/34,
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of CD40 expression
FH Key Location/Qualifiers
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Db 23 GAACAGAGAGACACACTGCCACC 1
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LOCUS          23 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Identification of genetic targets for modulation by
                oligonucleotides and generation of oligonucleotides for gene
                modulation.
ACCESSION      BD250532
VERSION        BD250532.1 GI:33060302
KEYWORDS       JP 2002511276-A/86.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Cowsett,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
                Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE          Identification of genetic targets for modulation by
                oligonucleotides and generation of oligonucleotides for gene
                modulation
JOURNAL        Patent: JP 2002511276-A 86 16-APR-2002;
COMMENT        ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002511276-A/86
                PD 16-APR-2002
                PF 13-APR-1999 JP 2000543647
                PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
                LEX M COWSETT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
                M SASNOR,
                PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
                Borchers,
                PI TIMOTHY A VIKKARS
                PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
                C12N15/00
                CC PCR Primer
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Query Match      2.3%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 202 CAGAGTTCACTGAACCGAATGC 224
Db 1 CAGAGTTCACTGAACCGAATGC 23
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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 04:55:45 ; Search time 648 Seconds

(without alignment)

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Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 120 summaries

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11: geneseqn2003ds.*

12: geneseqn2004as.*

13: geneseqn2004bs.*

14: geneseqn2005s.*

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SUMMARIES

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2	50	5.0	50	6	ABZ02105 Human leu
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4	50	5.0	50	10	ADP10127 50-mer ol
5	33	3.3	40	8	ABT31837 Anti-CD40
6	28	2.8	28	6	ABK66384 Human gen
7	28	2.8	28	6	ABK66383 Human gen
8	27.4	2.7	41	3	AAA50914 Human CD4
9	27	2.7	27	13	ADT51360 Anti-huma
10	27	2.7	36	12	ADP20784 CD40ex-F1
11	26.8	2.7	33	12	ADP20785 CD40ex-F1
12	26.4	2.6	37	3	AAA50913 Human CD4
13	26	2.6	26	12	ADP12202 Tagman pr
14	25	2.5	25	2	AZ40939 Human CD4
15	25	2.5	25	3	AZ47772 Human CD4
16	25	2.5	25	14	ADY75649 Human CD4
17	25	2.5	33	10	ADC79171 Human CD4
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19	24.6	2.5	35	12	ADO26914 CD40 tran

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c 94 20.2 2.0 41 6 ABZ47471 Human ATP
c 95 20.2 2.0 50 6 ABZ02836 Human leu
c 96 20.2 2.0 50 6 ABZ04731 Human leu
c 97 20 2.0 20 2 ABZ04943 Human CD4
c 98 20 2.0 20 3 AAAS1859 Primer B
c 99 20 2.0 20 6 ABN80810 Human CD4
c 100 20 2.0 20 10 ADD01330 Human CD4
c 101 20 2.0 20 10 ADC79533 Human CD4
c 102 20 2.0 20 12 ADOS7907 Human CD4
c 103 20 2.0 20 12 ADP10791 Set 1 lef
c 104 20 2.0 20 12 ADP11122 Set 1 rig
c 105 20 2.0 20 12 ADP11706 Set 2 lef
c 106 20 2.0 20 12 ADP11954 Set 2 rig
c 107 20 2.0 20 37 14 ADX17057 Human ZAC
c 108 20 2.0 42 2 AAA23265 Integrin
c 109 20 2.0 42 2 AA92715 Human A-r
c 110 20 2.0 42 3 AAZ64624 Hairpin r
c 111 20 2.0 42 7 AEB76385 Hepatitis
c 112 20 2.0 45 6 ABS57483 Human par
c 113 19.8 2.0 24 6 ABS64330 Rat Gene
c 114 19.8 2.0 27 12 ADF91549 Human TNF
c 115 19.8 2.0 49 12 ADL06397 PCR prime
c 116 19.8 2.0 50 5 ABL00115 Human sil
c 117 19.8 2.0 50 5 ABL00088 Human sil
c 118 19.8 2.0 50 6 ABZ07360 Human leu
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c 120 19.8 2.0 50 10 ADG33420 Human DNA
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ALIGNMENTS

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RESULT 1
ABZ00117
ID ABZ00117 standard; DNA; 50 BP.
XX
AC ABZ00117;
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DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 108.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quettermous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
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XX 22-OCT-2001; 2001WO-US047856.
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XX 20-OCT-2000; 2000US-0241994P.
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XX 08-JUN-2001; 2001US-0296764P.
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XX (BIOC-) BIOCARDIA INC.
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XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 330; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
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XX Sequence 50 BP; 15 A; 11 C; 18 G; 6 T; 0 U; 0 Other;
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XX Query Match 5.0%; Score 50; DB 6; Length 50;
XX Best Local Similarity 100.0%; Pred. No. 0.00033;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 827 GGTCAACCCAGGAGTGGCAAGAGAGTGCATCTTCAGTGCAGGAGAGAC 876
DB 1 GGTCAACCCAGGAGTGGCAAGAGAGTGCATCTTCAGTGCAGGAGAGAC 50
RESULT 2
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ID ABZ02105 standard; DNA; 50 BP.
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AC ABZ02105;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 2096.
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KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quettermous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 392; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
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CC  rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX  Sequence 50 BP; 16 A; 8 C; 20 G; 6 T; 0 U; 0 Other;
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Query Match          5.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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AC  ADG33437;
XX
DT  26-FEB-2004 (first entry)
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DE  Human DNA probe used to monitor expression of diagnostic genes SegID761.
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KW  human; ss; autoimmune; chronic inflammatory disease; SLE;
KW  systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;
KW  Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;
KW  ulcerative colitis; primary sclerosing cholangitis; appendicitis;
KW  diverticulitis; primary biliary sclerosis; probe.
XX
OS  Homo sapiens.
XX
PN  WO2003090694-A2.
XX
PD  06-NOV-2003.
XX
PF  24-APR-2003; 2003WO-US013015.
XX
PR  24-APR-2002; 2002US-00131827.
XX
PA  (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI  Wohlgenuth J, Fry K, Woodward R, Ly N;
XX  WPI; 2003-877243/81.
XX
DR  Diagnosing or monitoring autoimmune and chronic inflammatory diseases,
XX  such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative
XX  colitis, psoriasis and asthma by detecting the expression level of one or
XX  more genes.
XX
PS  Claim 1; SEQ ID NO 761; 877pp; English.
XX
CC  This invention relates to novel methods for diagnosing and monitoring
XX  autoimmune and chronic inflammatory diseases. Specifically, it refers to
XX  the identification of genes that have a clinical utility as diagnostic
XX  tools for the management of, in particular, patients with systemic lupus
XX  erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the
XX  present invention describes a method for determining the levels of
XX  multiple differentially expressed genes of a patient, in a concerted
XX  manner, in order to achieve an improved diagnostic assay with sensitivity
XX  and specificity for the disease in question. As such, these genes are
XX  useful for the diagnosis of various other inflammatory disorders
XX  including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,
XX  ankylosing spondylitis, ulcerative colitis, primary sclerosing
XX  cholangitis, appendicitis, diverticulitis, and primary biliary sclerosis.
XX  This oligonucleotide is a human DNA probe used to monitor the expression
XX  level of the differentially expressed diagnostic genes of the invention.
XX
SQ  Sequence 50 BP; 16 A; 8 C; 20 G; 6 T; 0 U; 0 Other;

Query Match          5.0%; Score 50; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  834 CAGGAGGATGGCAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 883
DB  1 CAGGAGGATGGCAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 50

RESULT 5
ABT31837
ID  ABT31837 standard; DNA; 40 BP.
```

```
OY  834 CAGGAGGATGGCAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 883
DB  1 CAGGAGGATGGCAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 50

RESULT 4
ADP10127
ID  ADP10127 standard; DNA; 50 BP.
AC  ADP10127;
XX
DT  12-AUG-2004 (first entry)
XX
DE  50-mer oligonucleotide marker probe of the invention #136.
XX
KW  transplant rejection; immune system; rheumatoid arthritis; lupus;
KW  inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS  Homo sapiens.
XX
PN  WO2004042346-A2.
XX
PD  21-MAY-2004.
XX
PF  24-APR-2003; 2003WO-US012946.
XX
PR  24-APR-2002; 2002US-00131831.
XX
PR  20-DEC-2002; 2002US-00325899.
XX
XX  (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI  Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX  Rosenberg S;
XX
DR  WPI; 2004-400724/37.
XX
PT  Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT  pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT  rejection, in an individual, comprises detecting the expression level of
PT  the genes.
XX
PS  Claim 2; SEQ ID NO 136; 1762pp; English.
XX
CC  The present invention relates to diagnosing or monitoring transplant
CC  rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC  comprises detecting the expression level of one or more genes. The
CC  methods, system and kits are useful in diagnosing or monitoring
CC  transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC  islet, lung, bone marrow or stem cell transplant rejection,
CC  xenotransplant rejection or mechanical organ replacement rejection, in an
CC  individual. The method is also useful in assessing the immune status of
CC  diseases that involve the immune system, e.g. rheumatoid arthritis,
CC  lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC  viral, bacterial or fungal infection. The present sequence represents a
CC  50 mer oligonucleotide marker for diagnosis and monitoring of allograft
CC  rejection and other disorders.
XX
SQ  Sequence 50 BP; 16 A; 8 C; 20 G; 6 T; 0 U; 0 Other;

Query Match          5.0%; Score 50; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  834 CAGGAGGATGGCAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 883
DB  1 CAGGAGGATGGCAAGAGAGTGGCATCTCAGTGCAGGAGAGACAGTGAGG 50

RESULT 5
ABT31837
ID  ABT31837 standard; DNA; 40 BP.
```



```
PD 05-MAR-2002.
XX
XX
XX 05-JAN-1999; 99US-00225928.
XX
XX 21-MAY-1997; 97US-00859998.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Chenchik A, Johhadze G, Bibilashvili R;
XX
XX WPI; 2002-314699/35.
XX
XX Producing sub-population of labeled nucleic acids, useful for analyzing
XX differences in RNA profiles between several different physiological
XX sources, using set of distinct gene specific primers.
XX
XX Example 3; SEQ ID NO 471; 11pp; English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
XX acids (NAs) comprising contacting a NA sample from a physiological
XX source, with a pool of 50 distinct gene specific primers under suitable
XX conditions to enzymatically generate sub-population of NAs, where each
XX gene specific primer has a sequence complementary to a distinct mRNA, and
XX each labeled NA is generated using a single gene specific primer. The
XX method is useful for producing a sub-population of labeled NAs which is
XX useful for analysing the differences in the RNA profiles between several
XX different physiological sources, where the method comprises producing
XX subpopulation of labeled NAs for the different physiological sources,
XX comprising the populations for each physiological source to identify
XX differences in the population, where the comparison is preferably
XX performed by hybridising the labeled NAs for each of the distinct
XX physiological sources to an array of probes NAs stably associated with the
XX surface of a substrate to produce a hybridisation pattern for each of the
XX sources, and comparing the patterns for each of the sources, where
XX differential gene expression assays are utilised in differential
XX expression analysis of diseased a normal tissue e.g. neoplastic a normal
XX tissue, or different tissue or sub-tissue types. The present sequence is a
XX human gene specific PCR primer used in the method of the invention. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX at http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1
XX
XX Sequence 28 BP; 9 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.8%; Score 28; DB 6; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 5.9e+02;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 198 TGCACAGAGTTCACTGAAACGGAATGCC 225
XX Db 1 TGCACAGAGTTCACTGAAACGGAATGCC 28
XX
XX RESULT 8
XX AAA50914/C
XX ID AAA50914 standard; DNA; 41 BP.
XX
XX AC AAA50914;
XX
XX 17-OCT-2000 (first entry)
XX
XX Human CD40 cytoplasmic domain PCR primer # 2.
XX
XX Human; TRAF protein; Tumour-necrosis factor; TNF; CD40; PCR primer; ss;
XX TNF receptor-associated factor; cell proliferation; cell differentiation;
XX apoptosis; inflammation; immune response; receptor-ligand binding assay.
XX
XX Homo sapiens.
XX
XX WO200026670-A1.
XX
XX 11-MAY-2000.
XX
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PF 23-AUG-1999; 99WO-US019272.
XX
XX 29-OCT-1998; 98US-00181958.
XX
XX (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
XX Kehry MR, Pullen SS, Crute JJ;
XX
XX WPI; 2000-451628/39.
XX
XX Quantitative assay for measuring the effect of a substance on tumor
XX necrosis factor receptor associated factor protein interaction with it
XX receptor.
XX
XX Example 1; Page 7; 27pp; English.
XX
XX Tumour necrosis factor (TNF) receptor has an important role in the
XX regulation of cellular proliferation, differentiation, and apoptosis in
XX inflammatory and immune responses. The present invention relates to a
XX quantitative assay for measuring the ability of a substance to effect
XX binding of a TNF receptor-associated factor (TRAF) protein to its
XX receptor. CD40 is a TRAF2 receptor. The present sequence is a PCR primer
XX used to amplify amino acids 216 to 277 of human CD40 cytoplasmic domain
XX (CD40c). Peptide antagonists of CD40c-TRAF2 binding were identified by
XX the present invention (AAB07004 to AAB07010)
XX
XX Sequence 41 BP; 7 A; 14 C; 9 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 27.4; DB 3; Length 41;
XX Best Local Similarity 96.6%; Pred. No. 1e+03;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 855 CGCATCTCAGTGCAGGAGACAGACGTGAGG 883
XX Db 41 CGCATCTCAGTGCAGGAGACAGACGTGATG 13
XX
XX RESULT 9
XX ADT51360
XX ID ADT51360 standard; RNA; 27 BP.
XX
XX AC ADT51360;
XX
XX 13-JAN-2005 (first entry)
XX
XX Anti-human CD40 gene small interfering RNA molecule #13.
XX
XX ds: immunosuppressive; antiinflammatory; antiallergic;
XX cardiovascular-Gen; antimicrobial; virucide; antibacterial;
XX antirheumatic; cytostatic; dermatologic; antipsoriatic;
XX antiarteriosclerotic; neuroprotective; antiasthmatic; antidiabetic;
XX antiulcer; thyromimetic; antiarthritic; respiratory-Gen;
XX gastrointestinal-Gen; gene therapy; human; CD40 receptor;
XX organ transplant rejection; inflammation; lymphocyte co-stimulation;
XX allergy; autoimmune disorder; cardiovascular disorder; rheumatoid state;
XX cancer; allergic dermatitis; psoriasis; arteriosclerosis;
XX multiple sclerosis; pulmonary fibrosis; asthma; diabetes; Lyme disease;
XX Crohn's disease; ulcerative colitis; lupus; thyroiditis; arthritis;
XX leukemia; lymphoma; neurodegenerative disease; small interfering RNA;
XX siRNA; gene expression; gene silencing.
XX
XX Synthetic.
XX
XX WO2004090134-A1.
XX
XX 21-OCT-2004.
XX
XX 15-MAR-2004; 2004WO-ES000117.
XX
XX 08-APR-2003; 2003ES-00000822.
XX
XX (PERR/) ARAN PERRAMON J M.
XX (BOIR/) GRINYO BOIRA J M.
XX
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PA (AMBR//) TORRAS AMBROS J.
PA (ORTE//) PLUVINET ORTEGA R.
PA (GARR//) CRUZADO GARRIT J M.
PA (FRES//) HERRERO FRESNEDA I.
XX
PI Aran Perramon JM, Grinyo Boira JM, Torras Ambros J;
PI Pluvinet Ortega R, Cruzado Garrit JM, Herrero Freshneda I;
XX
DR WPI; 2004-748766/73.
XX
XX New oligoribonucleotides specific for the human CD40 receptor, useful for
PT treating e.g. transplant rejection, inflammation and autoimmune diseases,
PT also related duplexes and gene transfer vectors.
XX
XX Disclosure; SEQ ID NO 13; 52pp; Spanish.
XX
CC The invention relates to oligoribonucleotide (ON1) homologous with the
CC 241-259 region of the cDNA (I) that encodes the human CD40 receptor,
CC published as GenBank X60592. ON1, also their subsequences and derived
CC duplexes (all optionally chemically modified), are useful for treatment
CC of rejection of transplanted organs or tissues; acute and chronic
CC inflammation; processes that involve co-stimulation of lymphocytes;
CC allergic, autoimmune or cardiovascular disorders; infections; rheumatoid
CC states and cancers, specifically allergic dermatitis; psoriasis;
CC arteriosclerosis; multiple sclerosis; pulmonary fibrosis; viral and
CC bacterial infection; asthma; type I diabetes; Lyme and Crohn diseases;
CC ulcerative colitis; lupus; thyroiditis; arthritis; leukemia and lymphoma;
CC also neurodegenerative diseases. This sequence corresponds to one of the
CC small interfering RNA (siRNA) molecules used as an example of the
CC oligonucleotides of the invention.
XX
SQ Sequence 27 BP; 10 A; 7 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 2.7%; Score 27; DB 13; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 237 GAAAGCGAATTCCTAGACACCTGGAC 263
Db 1 GAAAGCGAATTCCTAGACACCTGGAC 27

RESULT 10
ADP20784
ID ADP20784 standard; DNA; 36 BP.
XX
AC ADP20784;
XX
XX 12-AUG-2004 (first entry)
XX
DE CD40ex-Flag-TRAILex PCR primer 1160.
XX
XX ss; binding domain; cell-surface molecule; tumour necrosis factor;
KW TNF ligand family; TRAIL; TNF receptor superfamily; cytostatic;
KW antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
KW neuroprotective; antidiabetic; protozoacide; virucide; antibacterial;
KW antiallergic; signalling cascade; apoptosis; immunomodulation; cancer;
KW metabolic disease; multiple sclerosis; diabetes mellitus;
KW transplant rejection.
XX
OS Synthetic.
XX
XX DE10247755-A1.
XX
XX 22-APR-2004.
XX
XX 14-OCT-2002; 2002DE-01047755.
XX
XX 14-OCT-2002; 2002DE-01047755.
XX
XX (PFIZ//) PFIZENMAIER K.
XX (WAJA//) WAJANT H.
XX
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PI Pflizenmaier K, Wajant H;
XX
DR WPI; 2004-331870/31.
XX
XX New fusion polypeptide, useful for treating e.g. cancer, infections and
PT inflammation, comprises binding domain for cell-surface molecule and
PT fragment of tumor necrosis factor ligand.
XX
XX Example 1; Page 9; 16pp; German.
XX
XX This invention describes a novel polypeptide which comprises a segment
CC that contains a binding domain for a cell-surface molecule; a peptide
CC linker and a segment that contains a fragment of a member of the tumour
CC necrosis factor (TNF) ligand (TRAIL) family that, alone, is inactive or
CC has limited activity. The binding domain is not derived from an
CC immunoglobulin and the TRAIL fragment becomes fully active only after
CC binding of the binding domain to a cell-surface molecule. The TNF ligand
CC fragment is the extracellular domain (or its functional variants or
CC fragments) of a TNF family ligand, especially TRAIL, Fas, TNF, 41BBL,
CC CD40L, CD30L or OX40L. The binding domain binds to a membrane protein and
CC is at least the essential part of a ligand for a membrane-bound receptor,
CC specifically where the ligand is a peptide or protein hormone (especially
CC a growth factor, e.g. epidermal growth factor, or an angiogenic agent,
CC e.g. vascular endothelial growth factor) or a cytokine. Alternatively,
CC the binding domain is derived from a receptor, especially of the TNF
CC receptor superfamily, e.g. TNF-R2, CD30, CD40 or CD28, for a membrane-
CC bound ligand, provided that it does not bind to the extracellular domain
CC of the ligand from which TNF ligand segment is derived. The products of
CC the invention have cytostatic, antiinflammatory, immunosuppressive,
CC antirheumatic, antiarthritic, neuroprotective, antidiabetic,
CC protozoacide, virucide, antibacterial and antiallergic activity.
CC Activation of signalling cascades through TNF family receptors,
CC especially induction of apoptosis and immunomodulation. The polypeptide
CC of the invention, also nucleic acid constructs, vectors and cells that
CC express them, are useful for treatment of cancers (solid or lymphatic
CC tumours), metabolic diseases, inflammation and autoimmune diseases,
CC particularly rheumatic/arthritic diseases, also multiple sclerosis,
CC diabetes mellitus, protozoal, bacterial and viral infections and
CC transplant rejection. The effect of the TNF family ligand is developed in
CC targeted, tissue- or cell-specific manner, so adverse systemic side
CC effects are avoided, or at least much reduced.
XX
SQ Sequence 36 BP; 4 A; 14 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 CTCGCCATGTTCTGCTGCTCTGCTGCGAG 68
Db 10 CTCGCCATGTTCTGCTGCTCTGCTGCGAG 36

RESULT 11
ADP20785/C
ID ADP20785 standard; DNA; 33 BP.
XX
AC ADP20785;
XX
XX 12-AUG-2004 (first entry)
XX
DE CD40ex-Flag-TRAILex PCR primer 1161.
XX
XX ss; binding domain; cell-surface molecule; tumour necrosis factor;
KW TNF ligand family; TRAIL; TNF receptor superfamily; cytostatic;
KW antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
KW neuroprotective; antidiabetic; protozoacide; virucide; antibacterial;
KW antiallergic; signalling cascade; apoptosis; immunomodulation; cancer;
KW metabolic disease; multiple sclerosis; diabetes mellitus;
KW transplant rejection.
XX
OS Synthetic.
XX
```



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XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;  
PI Rosenberg S;  
XX WPI; 2004-400724/37.  
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,  
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant  
PT rejection, in an individual, comprises detecting the expression level of  
PT the genes.  
XX  
XX Claim 58; SEQ ID NO 2211; 1762pp; English.  
XX The present invention relates to diagnosing or monitoring transplant  
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual  
CC comprises detecting the expression level of one or more genes. The  
CC methods, system and kits are useful in diagnosing or monitoring  
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic  
CC islet, lung, bone marrow or stem cell transplant rejection,  
CC xenotransplant rejection or mechanical organ replacement rejection, in an  
CC individual. The method is also useful in assessing the immune status of  
CC an individual. The methods are also useful in diagnosing and monitoring  
CC diseases that involve the immune system, e.g. rheumatoid arthritis,  
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or  
CC viral, bacterial or fungal infection. The present sequence represents a  
CC probe for a 50 mer oligonucleotide marker for diagnosis and monitoring of  
CC allograft rejection and other disorders.  
XX  
XX Sequence 26 BP; 1 A; 6 C; 7 G; 12 T; 0 U; 0 Other;  
SQ Query Match 2.6%; Score 26; DB 12; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 692 CAAAAGGTGCGCCAAAGCCACCA 717  
Db 26 CAAAAGGTGCGCCAAAGCCACCA 1  
|||||  
RESULT 14  
AAZ40939  
ID AAZ40939 standard; DNA; 25 BP.  
XX  
XX AAZ40939;  
DT 26-JAN-2000 (first entry)  
XX  
DE Human CD40 PCR probe SEQ ID NO:88.  
XX  
XX Identification; genetic target; gene modulation; human; probe;  
KW antisense oligonucleotide; phosphorothioate; PCR primer;  
KW nucleotide sequence-based technology; antisense drug discovery;  
KW target validation; ss.  
XX  
XX Synthetic.  
OS  
OS Homo sapiens.  
XX  
XX WO9953101-A1.  
XX  
XX 21-OCT-1999.  
XX  
XX 13-APR-1999; 99WO-US008268.  
XX  
XX 13-APR-1998; 98US-0081483P.  
XX  
XX 28-APR-1998; 98US-00067638.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;  
PI Onasi C, Wyatt JR, Borchers AH, Vickers TA;  
XX WPI; 1999-620446/53.  
XX
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```
PT Identifying compounds which modulate expression of nucleic acids, used to  
PT provide compounds having defined physical, chemical or bioactive  
XX properties, e.g. antisense activity.  
XX Example 10; Page 84; 264pp; English.  
XX  
XX A method has been developed of defining a set of compounds that modulate  
CC the expression of a target nucleic acid (tNA) sequence via binding of the  
CC compounds with the tNA sequence. The method comprises generating a  
CC library of virtual compounds in silico according to defined criteria, and  
CC evaluating in silico the binding of the virtual compounds with the tNA  
CC according to defined criteria. Also described are: (1) a method of  
CC defining a set of oligonucleotides (ONs) that modulate the expression of  
CC a tNA sequence via binding of the ONs with the tNA sequence comprising  
CC generating a library of virtual compounds in silico according to defined  
CC criteria, and evaluating in silico the binding of the virtual ONs with  
CC the tNA according to defined criteria; and (2) a method of defining a set  
CC of compounds that modulate the expression of a tNA sequence via binding  
CC of the compounds with the tNA. The methods can be used for the generation  
CC and identification of synthetic compounds having defined physical,  
CC chemical or bioactive properties. Information gathered from assays of  
CC such compounds is used to identify nucleic acid sequences that are  
CC tractable to a variety of nucleotide sequence-based technologies, e.g.  
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and  
CC AAY52701 to AAY52706, represent sequences used in the exemplification of  
CC the present invention.  
XX  
XX Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;  
SQ Query Match 2.5%; Score 25; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 226 TTCTTTCGCGTGAAGCGAATTCCT 250  
Db 1 TTCTTTCGCGTGAAGCGAATTCCT 25  
|||||  
RESULT 15  
AAZ47772  
ID AAZ47772 standard; DNA; 25 BP.  
XX  
XX AAZ47772;  
DT 02-MAR-2000 (first entry)  
XX  
DE Human CD40 PCR probe SEQ ID NO:88.  
XX  
XX Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;  
KW expression; immune disease; inflammatory disease; immunomodulatory;  
KW anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;  
KW anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;  
KW hyperproliferative disease; autoimmune disease; rheumatoid arthritis;  
KW inflammatory bowel disease; asthma; psoriasis; cancer; tumour; PCR;  
KW probe; ss.  
XX  
XX Synthetic.  
OS  
OS Homo sapiens.  
XX  
XX WO9957320-A1.  
XX  
XX 11-NOV-1999.  
XX  
XX 22-APR-1999; 99WO-US008765.  
XX  
XX 01-MAY-1998; 98US-00071433.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Bennett CF, Cowsert LM;  
XX WPI; 2000-062158/05.  
XX
```

PT Antisense molecules directed against nucleic acid encoding human CD40,
 XX for treating e.g. immune, inflammatory or hyperproliferative diseases.
 PS Example 14; Page 52; 102pp; English.
 XX AA247685 to AA247768 represent phosphorothioate antisense
 CC oligonucleotides targeted to human CD40, which can be used to inhibit the
 CC expression of human CD40. CD40 is involved in lymphocyte activation,
 CC tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
 CC prevent immune-associated diseases (specifically guest vs. host disease,
 CC allograft rejection or autoimmune diseases); inflammation (specifically
 CC asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
 CC disease or psoriasis) or hyperproliferation (specifically cancer and
 CC tumours). the antisense oligonucleotides are also useful as diagnostic
 CC and research reagents. AA247769 represents the human CD40 nucleotide
 CC sequence. AA247770 to AA247772 represent human CD40 forward and reverse
 CC PCR primers, and a human CD40 PCR probe, respectively. AA247773 to
 CC AA247775 represent other PCR primers and a probe used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 2.5%; Score 25; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 226 TTCCTTCGGGTGAAGCGAATTCCT 250
 Db 1 TTCCTTCGGGTGAAGCGAATTCCT 25
 RESULT 16
 ADY75649
 ID ADY75649 standard; DNA; 25 BP.
 XX
 AC ADY75649;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Human CD40 RT-PCR probe.
 XX
 KW RT-PCR; probe; ss; diagnosis; drug discovery; mass spectroscopy;
 KW reverse transcriptase PCR; CD40.
 XX
 OS Homo sapiens.
 XX
 PN WO2005023986-A2.
 XX
 PD 17-MAR-2005.
 XX
 PF 07-SEP-2004; 2004WO-US028879.
 XX
 PR 04-SEP-2003; 2003US-0500723P.
 PR 04-SEP-2003; 2003US-0500724P.
 PR 04-SEP-2003; 2003US-0500730P.
 PR 04-SEP-2003; 2003US-0500732P.
 PR 04-SEP-2003; 2003US-0500824P.
 PR 11-SEP-2003; 2003US-0502007P.
 PR 11-SEP-2003; 2003US-0502076P.
 PR 17-SEP-2003; 2003US-0504495P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Griffey RH, Bennett CF, Ecker DJ, Ward DT, Freier SM;
 XX
 DR WPI; 2005-233282/24.
 XX
 PT Selecting a target molecule having affinity for a ligand that is equal
 PT to/greater than a baseline affinity by introducing a target molecule into
 PT a ligand and standard target test mixture and identifying complex by mass
 PT spectrometer.
 XX
 PS Example 65; SEQ ID NO 154; 314pp; English.

XX
 CC The invention relates to selecting a target molecule that has an affinity
 CC for a ligand that is equal to or greater than a baseline affinity,
 CC comprises introducing a target molecule into a test mixture of the ligand
 CC and a standard target, introducing the test mixture into a mass
 CC spectrometer and identifying any complexes of the target molecule and the
 CC ligand. Also included are a method of detecting a ligand-target complex
 CC having an affinity as expressed as a dissociation constant of nanomolar-
 CC 100 millimolar, a method for determining the relative interaction between
 CC at least two molecules determining target a ligand, a method of
 CC determining binding interaction (between a first target molecule and a
 CC second target molecule with respect to a ligand), a method of determining
 CC the relative proximity of binding sites for a first target molecule and a
 CC second target molecule on a ligand, a method of determining the relative
 CC orientation of a first target molecule to a second target molecule when
 CC bound to a ligand, a method for screening target molecules having binding
 CC affinity to a ligand, a method for modulating the binding affinity of a
 CC target molecule for a ligand, a method for refining the binding of a
 CC target molecule to a ligand, a method of favoring an alternate structure
 CC of an oligomer, a method for identifying a ligand that alters a target
 CC compound secondary structure, a method of determining the relative change
 CC in proximity of binding sites for a first ligand and a second ligand on a
 CC target substrate influenced by the first ligand, a method of determining
 CC the relative change in proximity of a first binding site for a binding
 CC ligand and a second binding site for a second binding ligand on a target,
 CC a method of determining the relative orientation of a first ligand to a
 CC second ligand when bound to a target substrate, an oligomeric compound
 CC comprising a nucleotide sequence at least 80% complementary to a target
 CC RNA (where the oligomeric compound comprises 21-24 nucleotides, and
 CC comprises a nucleotide sequence that corresponds to a portion of the
 CC nucleotide sequence of a larger oligomeric compound that comprises a
 CC stemloop structure), a method of modulating transcription in a cell, a
 CC method of modulating translation in a cell, a method of modulating a
 CC conversion of a precursor RNA into a microRNA in a cell, a method of
 CC generating a set of (oligomeric) compounds that modulate the expression
 CC of a target nucleic acid molecule, a computer formatted medium comprising
 CC computer readable instructions for identifying active compounds or for
 CC performing the method above, a method of predicting evolutionarily
 CC allowed mutations of a microRNA, a method of grouping biological members
 CC according to a grouping criteria, a method of determining a blur-factor
 CC and a method of determining a group of probable mutations for a microRNA.
 CC The methods of the invention may be applied to the design of siRNA (short
 CC interfering RNA) and antisense oligonucleotides. The method is useful for
 CC determining the mode of binding interaction between two or more target
 CC molecules to the ligand as well as their relative affinities. The
 CC oligomeric compounds are useful in drug discovery and target validation,
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
 CC The present sequence is an RT-PCR (reverse transcriptase PCR) probe for
 CC human CD40 mRNA used to assess expression of CD40 during treatment with
 CC antisense oligonucleotides targeted to the human CD40 gene, designed
 CC according to the methods of the invention.
 XX
 SQ Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 2.5%; Score 25; DB 14; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 226 TTCCTTCGGGTGAAGCGAATTCCT 250
 Db 1 TTCCTTCGGGTGAAGCGAATTCCT 25
 RESULT 17
 ADC79171
 ID ADC79171 standard; DNA; 33 BP.
 XX
 AC ADC79171;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human CD40 forward PCR primer.
 XX

PT inhibition of apoptosis caused by binding of FBM to second binding pair
PT member.
XX Example 1; Page 32; 84pp; English.
XX
CC The present invention relates to a method for identifying members of
CC specific binding pairs. The method comprises providing a cell which is
CC susceptible to apoptosis, expressing in the cell a first binding pair
CC member (FBM) fused to apoptosis inhibitor, exposing the cell to an
CC apoptosis inducing agent and contacting the cell with a second binding
CC pair member (SBM), where members of specific binding pairs are identified
CC by binding of FBM to SBM, such that apoptosis inhibitor is activated to
CC inhibit apoptosis. The method is useful for screening human cDNA
CC libraries for target antigens e.g., tumour epitopes. Preferably, the FBM
CC are expressed as fusion proteins with the signalling portion (the
CC transmembrane and cytoplasmic) of CD40 (CD40t/c). The present sequence is
CC a PCR primer used in an example from the invention.
XX
SQ Sequence 35 BP; 6 A; 13 C; 8 G; 8 T; 0 U; 0 Other;
XX
Query Match 2.5%; Score 24.6; DB 12; Length 35;
Best Local Similarity 87.1%; Pred. No. 6.3e+03;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 859 TCTCAGTCGAGAGACAGTCAGCTGCAC 889
DB 35 TCTCAGTCGAGAGACAGTCAGTCGACG 5
XX
RESULT 20
ADO26923/c
ID ADO26923 standard; DNA; 35 BP.
XX
AC ADO26923;
XX
DT 12-AUG-2004 (first entry)
XX
DE CD40 variant PCR primer G.
XX
KW CD40 transmembrane domain; CD40 cytoplasmic domain; CD40; CD40t/c; PCR;
KW primer; ss.
XX
OS Synthetic.
XX
FN GB2395554-A.
XX
PD 26-MAY-2004.
XX
PF 19-NOV-2002; 2002GB-00026909.
XX
PR 19-NOV-2002; 2002GB-00026909.
XX
PA (ALLI-) ALLIGATOR BIOSCIENCE AB.
XX
PI Ellmark P, Furebring C, Ohlin M, Borrebaeck CAK;
XX
DR WPI; 2004-422835/40.
XX
PT Identifying members of specific binding pairs in cell expressing first
PT binding pair member (FBM) fused to apoptosis inhibitor by identifying
PT inhibition of apoptosis caused by binding of FBM to second binding pair
PT member.
XX
PS Example 2; Page 51; 84pp; English.
XX
CC The present invention relates to a method for identifying members of
CC specific binding pairs. The method comprises providing a cell which is
CC susceptible to apoptosis, expressing in the cell a first binding pair
CC member (FBM) fused to apoptosis inhibitor, exposing the cell to an
CC apoptosis inducing agent and contacting the cell with a second binding
CC pair member (SBM), where members of specific binding pairs are identified
CC by binding of FBM to SBM, such that apoptosis inhibitor is activated to
CC inhibit apoptosis. The method is useful for screening human cDNA

CC libraries for target antigens e.g., tumour epitopes. Preferably, the FBM
CC are expressed as fusion proteins with the signalling portion (the
CC transmembrane and cytoplasmic) of CD40 (CD40t/c). The present sequence is
CC a PCR primer used in an example from the invention.
XX
SQ Sequence 35 BP; 6 A; 13 C; 8 G; 8 T; 0 U; 0 Other;
XX
Query Match 2.5%; Score 24.6; DB 12; Length 35;
Best Local Similarity 87.1%; Pred. No. 6.3e+03;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 859 TCTCAGTCGAGAGACAGTCAGCTGCAC 889
DB 35 TCTCAGTCGAGAGACAGTCAGTCGACG 5
XX
RESULT 21
AAA51858
ID AAA51858 standard; DNA; 24 BP.
XX
AC AAA51858;
XX
DT 31-OCT-2000 (first entry)
XX
DE Primer A for porcine CD40 cDNA amplification.
XX
KW CD40 antigen; xenograft; CD40-deficient donor; graft rejection;
KW transgenic pig; reduced immunogenicity; immunosuppressive; gene therapy;
KW primer; ss.
XX
OS Homo sapiens.
OS Mus sp.
OS Bos taurus.
XX
FN WO200039294-A1.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-EP010332.
XX
PR 24-DEC-1998; 98GB-00028705.
PR 10-FEB-1999; 99GB-00002940.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Bravery C, Rushworth S, Thompson S;
XX
DR WPI; 2000-452392/39.
XX
PT Ameliorating cellular graft rejection in a recipient mammal using CD40-
PT deficient donor mammal cells, tissues or organs as a xenograft, comprises
PT inactivation of the CD40 antigen gene with a targeting vector.
XX
PS Example 1; Page 8; 23pp; English.
XX
CC Primers shown in AAA51858-59 were designed based on areas of sequence
CC conserved in the human, mouse and bovine CD40 genes. A fusion protein
CC consisting of the extracellular domain of human CD154 coupled to mouse Ig
CC kappa light chain was able to bind to porcine CD40, indicating that
CC direct signalling between a porcine graft and the immune cells of a human
CC host is possible through this molecular pathway. CD40-deficient donor
CC mammal cells, tissues or organs may be used for xenografting in order to
CC ameliorate cellular graft rejection in the recipient mammal. In
CC particular, porcine cells, tissues or organs are genetically modified so
CC that the cell surface expression of CD40 antigen is reduced. Transgenic
CC pigs may have an inactivated CD40 antigen gene and a transgene, e.g.
CC human Decay Accelerating Factor (hDAF) gene. The CD40-deficient donor
CC mammal cells, tissues or organs may be used as transplants (e.g. lung,
CC heart) in humans or other mammals (claimed). The transplants have a
CC reduced immunogenicity because the CD40 antigen gene is inactivated
XX
SQ Sequence 24 BP; 3 A; 7 C; 4 G; 10 T; 0 U; 0 Other;

```
Query Match      2.4%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 TCGGCTTCTTCTCCAAATGTGTCAT 513
DB 1 TCGGCTTCTTCTCCAAATGTGTCAT 24

RESULT 22
ABN80809
ID ABN80809 standard; DNA; 24 BP.
AC ABN80809;
XX
XX
DT 15-JUL-2002 (first entry)
DE Human CD40 PCR primer SEQ ID NO 27.
XX
KW Human; IRF-1; transcription factor; interferon regulatory factor;
KW antisense; gene therapy; cardiovascular; transplant rejection;
KW immunological hypersensitivity; asthma; inflammatory disease; psoriasis;
KW Crohn's disease; autoimmune disease; diabetes mellitus; Th2 response;
KW multiple sclerosis; rheumatoid arthritis; Th1 response; Th2 response;
KW vasotrophic; immunosuppressive; antiasthmatic; dermatological;
KW antiallergic; antiulcer; antiinflammatory; antipsoriatic; antidiabetic;
KW neuroprotective; antirheumatic; antiarthritic; PCR; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200229044-A2.
XX
XX 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-DE003835.
XX
XX 06-OCT-2000; 2000DE-01049549.
XX
XX 29-NOV-2000; 2000DE-01059144.
XX
XX (HECKER) HECKER M.
XX (WAGN) WAGNER A H.
XX
XX Hecker M, Wagner AH;
XX
XX WPI; 2002-383335/41.
XX
XX Inhibitor of the transcription factor IRF-1, useful for treating e.g.
XX transplant rejection and autoimmune disease, reduces expression of CD40.
XX
XX Example 2; Page 18; 45pp; German.
XX
XX The invention relates to an inhibitor (I) of the expression and/or
XX activity of the transcription factor (IRF-1; interferon regulatory
XX factor) as a therapeutic agent, especially an oligonucleotide inhibitor
XX (ABN80783-ABN80804) or antisense oligonucleotide (ABN80805-ABN80808) used
XX in antisense gene therapy. (I) are used to prevent or treat
XX cardiovascular complications such as restenosis after angioplasty or
XX stenosis of venous by-passes, chronic or acute transplant rejection and
XX graft versus host disease, immunological hypersensitivity, e.g. bronchial
XX asthma or atopic dermatitis, inflammatory diseases such as ulcerative
XX colitis, psoriasis and Crohn's disease and autoimmune diseases such as
XX diabetes mellitus, multiple sclerosis, collagenosis (e.g. systemic lupus
XX erythematosus), rheumatoid arthritis and vasculitis. (I) simultaneously
XX weaken both Th1 and Th2 responses. The present sequence is that of a PCR
XX primer, useful to the invention
XX
XX Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      2.4%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAACCGAATGCC 225
DB 1 CAGAGTTCACTGAACCGAATGCC 24

RESULT 23
ADA25646
ID ADA25646 standard; DNA; 24 BP.
AC ADA25646;
XX
XX
DT 20-NOV-2003 (first entry)
DE CD40 general forward primer #SEQ ID 18.
XX
KW CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
KW inflammatory disease; cancer; atherosclerosis; acute injury; PCR; primer;
KW ss.
XX
XX Homo sapiens.
XX
XX WO2003070768-A2.
XX
XX 28-AUG-2003.
XX
XX 24-FEB-2003; 2003WO-IB000665.
XX
XX 22-FEB-2002; 2002US-0358877P.
XX
XX (COMP-) COMPUGEN LTD.
XX
XX Bernstein J, Mintz L, Eshel D;
XX
XX WPI; 2003-697601/66.
XX
XX Protein, useful for preparing a composition for modulating CD40-CD154
XX interactions in an individual for treating chronic inflammatory disease,
XX cancer, atherosclerosis or acute injury.
XX
XX Disclosure; Page 89; 92pp; English.
XX
XX The invention relates to substantially pure CD40 splice variant proteins
XX which include tail sequences. Also disclosed is a pharmaceutical
XX composition comprising the protein and a carrier, an in vitro method of
XX detecting whether an individual is expressing the protein, and a method
XX for modulating CD40-CD154 interactions in an individual. The protein of
XX the invention is useful for preparing a composition for modulating CD40-
XX CD154 interactions in an individual for treating chronic inflammatory
XX disease, cancer, atherosclerosis or acute injury. The current sequence
XX represents a PCR primer for amplifying CD40 splice variant.
XX
XX Sequence 24 BP; 4 A; 5 C; 10 G; 5 T; 0 U; 0 Other;

Query Match      2.4%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGCACGTGTACGAGTGAGGCGCTGTG 396
DB 1 GGCACGTGTACGAGTGAGGCGCTGTG 24

RESULT 24
ADD01329
ID ADD01329 standard; DNA; 24 BP.
XX
XX ADD01329;
XX
XX
DT 01-JAN-2004 (first entry)
XX
XX Human CD40 PCR primer SEQ ID 44.
XX
```

ss; inhibitor; STAT-1; signal transducer and activator of transcription;
 KW cardiovascular; restenosis; percutaneous angioplasty; stenosis;
 KW graft versus host reaction; ischaemic injury; reperfusion injury;
 KW organ transplantation; immunological hypersensitivity; allergic rhinitis;
 KW immune complex disease; allergic vasculitis; arthritis; bone disease;
 KW glomerulonephritis; allergic vasculitis; gout; osteitis; osteomyelitis;
 KW polyneuritis; bronchitis; endocarditis; hepatitis; myocarditis;
 KW nephritis; pericarditis; peritonitis; pancreatitis; septic shock;
 KW vasotropic; immunosuppressive; anti-allergic; anti-inflammatory;
 KW dermatological; antiarthritic; neurotropic; antigout; osteopathic;
 KW hepatotropic; virucide; cardiac; antibacterial; human; CD40; PCR;
 KW primer.
 XX
 OS Homo sapiens.
 XX
 XX WO2003030944-A2.
 XX
 XX 17-APR-2003.
 XX
 XX 02-OCT-2002; 2002WO-DE003748.
 XX
 XX 04-OCT-2001; 2001DE-01048886.
 XX (AVON-) AVONTEC GMBH.
 XX
 XX Hecker M, Wagner AH;
 XX
 XX WPI; 2003-381684/36.
 DR
 XX
 XX Use of inhibitor of STAT-1 activity, for treating or preventing e.g.
 XX cardiovascular complications, graft versus host reactions or
 XX immunological hypersensitivity.
 PT
 PT Disclosure; SEQ ID NO 44; 53pp; German.

This invention describes the novel use of an inhibitor of STAT-1 (signal transducer and activator of transcription) for prevention or treatment of cardiovascular complications and other diseases e.g. restenosis after percutaneous angioplasty or stenosis in venous by-passes; graft versus host reactions; ischaemic/reperfusion injury in surgical operations or organ transplantation, immunological hypersensitivity reactions, especially allergic rhinitis, food and medicine allergies (particularly urticaria and celiac disease), contact dermatitis, immune complex diseases, especially alveolitis, arthritis, glomerulonephritis and allergic vasculitis, inflammatory cartilage and bone diseases (especially arthritis, gout, osteitis and osteomyelitis), polyneuritis, also (sub)acute infection-related, particularly post-infection, inflammatory conditions, particularly bronchitis, endocarditis, hepatitis, myocarditis, nephritis, pericarditis, peritonitis and pancreatitis, including septic shock. The inhibitor is a double-stranded (ds) DNA oligonucleotide which acts as a decoy, a single-stranded antisense oligonucleotide, an antisense expression vector or ds RNA-interference (RNAi) oligonucleotide. The products of the invention have vasotropic, immunosuppressive, anti-allergic, anti-inflammatory, dermatological, antiarthritic, nephrotropic, antigout, osteopathic, hepatotropic, virucide, cardiac and antibacterial activity. ADD01286-ADD01346 represent the STAT-1 decoy oligonucleotides used in the method of the invention.

Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACGAAACCGAATGCC 225
 |||||
 Db 1 CAGAGTTCACGAAACCGAATGCC 24

RESULT 25
 ADC79532

ID ADC79532 standard; DNA; 24 BP.
 XX
 AC ADC79532;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human CD40 PCR primer SEQ ID 44.
 XX
 KW vasotropic; anti-allergic; neuroprotective; immunosuppressive;
 KW antirheumatic; anti-inflammatory; dermatological; antiarthritic;
 KW antiasthmatic; antidiabetic; antipsoriatic; antibacterial; STAT-1;
 KW proinflammatory; leucocyte; endothelial cell; smooth muscle cell; CD40;
 KW E-selectin; inducible nitric oxide synthase; iNOS; interleukin-12;
 KW interferon-gamma; cardiovascular; restenosis; percutaneous angioplasty;
 KW transplant rejection; graft versus host disease; reperfusion;
 KW hypersensitivity reaction; autoimmune disease; diabetes mellitus;
 KW multiple sclerosis; rheumatoid arthritis; chronic inflammatory disease;
 KW arthritis; asthma; bronchitis; psoriasis; neurodermatitis;
 KW ulcerative colitis; Crohn's disease; primer; ss; PCR.
 XX
 OS Homo sapiens.
 XX
 XX WO2003031459-A2.
 XX
 XX 17-APR-2003.
 XX
 XX 02-OCT-2002; 2002WO-DE003747.
 XX
 XX 04-OCT-2001; 2001DE-01048828.
 XX (AVON-) AVONTEC GMBH.
 XX
 XX Hecker M, Wagner AH;
 XX
 XX WPI; 2003-363361/34.
 DR
 XX
 XX New decoy oligonucleotides, useful for treating and preventing e.g.
 XX cardiovascular complications or transplant rejection, by neutralization
 XX of STAT-1.
 PT
 PT Example 2; SEQ ID NO 44; 52pp; German.

This invention describes novel decoy oligonucleotides which have vasotropic, anti-allergic, neuroprotective, immunosuppressive, antirheumatic, anti-inflammatory, dermatological, antiarthritic, antiasthmatic, antidiabetic, antipsoriatic and antibacterial activity. The oligonucleotides neutralise or inhibit expression of STAT-1 and thus of a range of potentially proinflammatory gene products in leucocytes, endothelial and smooth muscle cells. Genes that have a STAT-1 binding site in their promoters include those for CD40, E-selectin, inducible nitric oxide synthase (NOS), interleukin-12 and interferon-gamma. Also the oligonucleotides of the invention may lift inhibition of gene expression where this is blocked by transcription factors, e.g. the gene for endothelial NOS which is down regulated by interferon-gamma. The decoy oligonucleotide and new antisense oligonucleotides, are used to treat or prevent cardiovascular complications, especially restenosis after percutaneous angioplasty and stenosis in venous by-passes, transplant rejection, graft versus host disease, ischaemic/reperfusion injuries of surgery, immunological hypersensitivity reactions (types I-V), autoimmune diseases (especially diabetes mellitus, multiple sclerosis and rheumatoid arthritis), all forms of (sub)acute or chronic inflammatory diseases, especially of the joints (arthritis), respiratory organs (bronchial asthma and chronic bronchitis), skin (psoriasis and neurodermatitis) or gastrointestinal tract (ulcerative colitis or Crohn's disease). ADC79489-ADC79549 represent the decoy oligonucleotides described in the disclosure of the invention.

Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225
Db 1 CAGAGTTCACCTGAAACGGAATGCC 24

RESULT 26
AC000576/c
ID ACC00576 standard; DNA; 24 BP.
XX
AC ACC00576;
XX
XX 23-JUN-2003 (first entry)
XX
XX Human CD40 DNA amplifying antisense primer.
XX
XX Kidney disease; transplantation; nephric tissue; nephrotropic;
XX cystostatic; litholytic; antidiabetic; thrombolytic; CD40; PCR; primer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO2003022123-A2.
XX
XX 20-MAR-2003.
XX
XX 01-SEP-2002; 2002WO-IL000722.
XX
XX 07-SEP-2001; 2001US-0317452P.
XX
XX 10-APR-2002; 2002US-00118933.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Reisner V, Dekel B;
XX
XX WPI; 2003-354496/33.
XX
XX Treating kidney disease e.g. chronic nephritis comprises transplanting
XX human or porcine nephric tissue graft transplantation at differentiation
XX stage corresponding to specific period of gestation.
XX
XX Example 1; Page 24; 54pp; English.
XX
XX The invention relates to treating a kidney disease and involves
XX transplanting a graft of human nephric tissue at a differentiation stage
XX corresponding to 4-10 weeks of gestation or transplanting a graft of
XX porcine nephric tissue at a differentiation stage corresponding to 3-6
XX weeks of gestation. The method is used for treating kidney disease and
XX for evaluating transplant suitability. The kidney disease includes acute
XX kidney failure, acute nephritic syndrome, analgesic nephropathy,
XX atherembolic renal disease, chronic kidney failure, chronic nephritis,
XX congenital nephrotic syndrome, end-stage renal disease, Goodpasture's
XX syndrome, IgM mesangial proliferative glomerulonephritis, interstitial
XX nephritis, kidney cancer, kidney damage, kidney infection, kidney injury,
XX kidney stones, lupus nephritis, membranoproliferative glomerulonephritis
XX I, membranoproliferative glomerulonephritis II, membranous nephropathy,
XX necrotizing glomerulonephritis, nephroblastoma, nephrocalcinosis,
XX nephrogenic diabetes insipidus, IgA-mediated nephropathy, nephrosis,
XX nephritic syndrome, polycystic kidney disease, post-streptococcal
XX glomerulonephritis, reflux nephropathy, renal artery embolism, renal
XX artery stenosis, renal papillary necrosis, renal tubular acidosis type I,
XX renal tubular acidosis type II, renal underperfusion and renal vein
XX thrombosis. Sequences ACC00575-76 represent PCR primers for amplifying
XX the human CD40 DNA
XX
XX Sequence 24 BP; 7 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.4%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 GCTACAGGGGTTTCTGATACATC 473
Db 24 GCTACAGGGGTTTCTGATACATC 1

us-10-698-689-85.sz1m50.rng

RESULT 27
ADO57906
ID ADO57906 standard; DNA; 24 BP.
XX
XX ADO57906;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human CD4U RT-PCR forward primer.
XX
XX immunosuppressive; vasotropic; double-stranded oligonucleotide;
XX transcription factor; AP-1; acute transplant rejection;
XX chronic transplant rejection; graft-versus-host disease;
XX ischaemic injury; reperfusion injury; surgery;
XX gene transcription modulation; reverse transcriptase PCR; RT-PCR; primer;
XX ss; human; CD4U.
XX
XX Homo sapiens.
XX
XX DE10240417-A1.
XX
XX 11-MAR-2004.
XX
XX 02-SEP-2002; 2002DE-01040417.
XX
XX 02-SEP-2002; 2002DE-01040417.
XX
XX (AVON-) AVONTEC GMBH.
XX
XX Hecker M, Wagner AH;
XX
XX WPI; 2004-228818/22.
XX
XX New double-stranded oligonucleotides that bind specifically to the AP-1
XX transcription factor, useful for treating e.g. transplant rejection or
XX ischemic/reperfusion injury.
XX
XX Disclosure; SEQ ID NO 37; 31pp; German.
XX
XX The invention describes double-stranded (ds) DNA oligonucleotides (I) in
XX which one strand (Ia) has any of 26 sequences (some degenerate), given in
XX the specification, and the other strand is complementary to (Ia). Also
XX described are the use of (a) ds oligonucleotides (II) that bind to the
XX transcription factor AP-1 or (b) ds oligonucleotides (III) having any of
XX 36 specified sequences (these include (i) for preparing a composition
XX for treatment or prevention of (i) acute or chronic transplant rejection
XX and graft-versus-host disease or (ii) ischaemic/reperfusion injury to
XX organs during surgery. (I), and other known ds oligonucleotides that bind
XX to the transcription factor AP-1, are used to treat or prevent (i) acute
XX or chronic transplant rejection and graft-versus-host disease or (ii)
XX ischaemic/reperfusion injury to organs during surgery. They are also used
XX to modulate gene transcription in cells, especially endothelial and
XX antigen-presenting cells, e.g. by ex vivo treatment of donor organs
XX before transplantation. (I) become active immediately after entering a
XX cell, i.e. more quickly than antisense or interfering oligonucleotides.
XX This sequence represents a reverse transcription PCR primer used in the
XX isolation of human CD4U, used in an assay to determine the effect of ds
XX oligonucleotides on AP-1 binding specificity.
XX
XX Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.4%; Score 24; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACCTGAAACGGAATGCC 225
Db 1 CAGAGTTCACCTGAAACGGAATGCC 24

RESULT 28

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XX PD 20-JAN-1994.
XX PF 08-JUL-1993; 93WO-US006432.
XX PR 09-JUL-1992; 92US-00910222.
XX PR 09-FEB-1993; 93US-00015147.
XX PR 28-MAY-1993; 93US-00070158.
XX PA (CETU) CETUS ONCOLOGY CORP.
XX PI De Boer M, Conroy LB;
XX DR WPI; 1994-035055/04.
XX PT Antibodies to membrane-associated antigens - used for treating transplant
PT rejection, graft-versus-host disease, antibody-mediated disease and auto-
PT immune disease.
XX PS Disclosure; Fig 2; 113pp; English.
XX CC Primers (AAQ55223-30) are used to amplify the human CD40 antigen and the
CC human B7 DNA. The CD40 antigen is immunoreactive with an anti- CD40 Mab.
CC The binding of the Mab to the CD40 antigen is located on the surface of a
CC human B cell. The antibodies can be used to treat transplant rejection
CC diseases as well as autoimmune infections. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 31
AAQ96203
ID AAQ96203 standard; DNA; 32 BP.
XX AC AAQ96203;
XX DT 26-MAR-1996 (first entry)
XX DE Primer #3.
XX KW Polymerase chain reaction; PCR; primer; amplify; B7; B-cell; T-cell;
KW baculovirus vector; hybridoma; antibody; antigen; immunosuppressor;
KW interleukin-2; IL-2; transplant rejection; graft vs host disease; GVHD;
KW rheumatoid arthritis; therapy; CD28; ss.
XX OS Synthetic.
XX PN WO9522619-A1.
XX PD 24-AUG-1995.
XX PF 19-JAN-1995; 95WO-US000897.
XX PR 18-FEB-1994; 94US-00200716.
XX PA (CETU) CETUS ONCOLOGY CORP.
XX PI De Boer M, Conroy LB;
XX DR WPI; 1995-302723/39.
XX CC T cell anergy induction by coadmin. of anti-B7-antibody and
PT immunosuppressive agent - used to prevent transplant rejection, and to
PT treat graft vs host disease and rheumatoid arthritis.

XX PS Disclosure; p57; 77pp; English.
XX CC The sequences represented by AAQ96201-Q96204 are used in the invention.
CC The sequences represented by AAQ96197 and AAQ96198 are primers for the
CC full length B7-1. This sequence is also used (along with AAQ96200) as a
CC primer for soluble B7-1. This sequence corresponds to bases 307-324 of
CC the full length B7 gene. B7 is a monomeric transmembrane glycoprotein
CC that is expressed on activated B-cells, and is a ligand for the CD28
CC receptor of T-cells. There are three ligands of B7 (B7-1, B7-2, and B7-
CC 3). The sequence amplified by these primers is inserted into a
CC baculovirus vector and used for the production of B7-1 specific
CC antibodies using hybridoma techniques. The anti-B7-1 antibodies can then
CC be included in a composition containing an immunosuppressive agent that
CC inhibits the production of interleukin-2 (IL-2) by T-cells. This
CC composition can be administered to patients and thereby used to prevent
CC transplant rejection, and to treat graft vs host disease (GVHD) and
CC rheumatoid arthritis. The advantage with using this composition is that
CC it induces long-lasting T-cell anergy against an alloantigen
XX SQ Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 CTGGTCTCACCTCGCCATGGTTTCG 55
Db 9 CTGGTCTCACCTCGCCATGGTTTCG 32

RESULT 32
AAQ96201
ID AAQ96201 standard; DNA; 32 BP.
XX AC AAQ96201;
XX DT 26-MAR-1996 (first entry)
XX DE Primer #1.
XX KW Polymerase chain reaction; PCR; primer; amplify; B7; B-cell; T-cell;
KW baculovirus vector; hybridoma; antibody; antigen; immunosuppressor;
KW interleukin-2; IL-2; transplant rejection; graft vs host disease; GVHD;
KW rheumatoid arthritis; therapy; CD28; ss.
XX OS Synthetic.
XX PN WO9522619-A1.
XX PD 24-AUG-1995.
XX PF 19-JAN-1995; 95WO-US000897.
XX PR 18-FEB-1994; 94US-00200716.
XX PA (CETU) CETUS ONCOLOGY CORP.
XX PI De Boer M, Conroy LB;
XX DR WPI; 1995-302723/39.
XX CC T cell anergy induction by coadmin. of anti-B7-antibody and
PT immunosuppressive agent - used to prevent transplant rejection, and to
PT treat graft vs host disease and rheumatoid arthritis.
XX PS Disclosure; p56; 77pp; English.
XX CC The sequences represented by AAQ96201-Q96204 are used in the invention.
CC The sequences represented by AAQ96197 and AAQ96198 are primers for the
CC full length B7-1. This sequence is also used (along with AAQ96200) as a
CC primer for soluble B7-1. This sequence corresponds to bases 307-324 of
CC the full length B7 gene. B7 is a monomeric transmembrane glycoprotein

CC that is expressed on activated B-cells, and is a ligand for the CD28
 CC receptor of T-cells. There are three ligands of B7 (B7-1, B7-2, and B7-
 CC 3). The sequence amplified by these primers is inserted into a
 CC baculovirus vector and used for the production of B7-1 specific
 CC antibodies using hybridoma techniques. The anti-B7-1 antibodies can then
 CC be included in a composition containing an immunosuppressive agent that
 CC inhibits the production of interleukin-2 (IL-2) by T-cells. This
 CC composition can be administered to patients and thereby used to prevent
 CC transplant rejection, and to treat graft vs host disease (GVHD) and
 CC rheumatoid arthritis. The advantage with using this composition is that
 CC it induces long-lasting T-cell anergy against an alloantigen
 XX
 SQ Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCGCATGGTTTCG 55
 |||||
 Db 9 CTGGTCTCACCTCGCGCATGGTTTCG 32

RESULT 33
 AAT79188
 ID AAT79188 standard; DNA; 32 BP.

XX
 AC AAT79188;
 XX
 DT 23-MAR-1998 (first entry)
 XX
 DE Human soluble CD40 antigen PCR primer.

XX Human; B7 antigen; CD40; PCR primer; monoclonal antibody; B cell; growth;
 KW differentiation; allergy; autoimmune disease; ss.
 XX
 OS Synthetic.

XX
 PN WO9731025-A1.
 XX
 PD 28-AUG-1997.

XX
 PF 21-FEB-1997; 97WO-US002858.
 XX
 PR 23-FEB-1996; 96US-00606293.

XX
 PA (CHIR) CHIRON CORP.
 XX
 PI De Boer M;

XX
 DR WPI; 1997-435094/40.
 XX

XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
 PT prevent their growth and differentiation, useful to treat or prevent
 PT antibody mediated allergies and autoimmune diseases.

XX Example 1; Fig 2; 64pp; English.

XX A novel humanised monoclonal antibody (MAB) has been developed which: (a)
 CC binds a human CD40 antigen on the surface of a B cell, to prevent its
 CC growth and differentiation; and (b) has an effective number of exposed
 CC amino acids in its framework regions that are consistent with amino acid
 CC residues found in the corresponding framework regions of a human Ab to
 CC provide a reduced immunogenicity in humans. The present sequence
 CC represent a PCR primer used in an example of the present invention. The
 CC MAB can be used to prevent or treat antibody mediated diseases,
 CC particularly immunoglobulin E (IgE) mediated allergies, systemic lupus
 CC erythematosus, primary biliary cirrhosis, idiopathic thrombocytopenia
 CC purpura and rheumatoid arthritis. The MAB inhibits the normal B cell
 CC response to CD40 ligands at relatively low concentrations and is unlikely
 CC to cause any immune response in humans

XX Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCGCATGGTTTCG 55
 |||||
 Db 9 CTGGTCTCACCTCGCGCATGGTTTCG 32

RESULT 34
 AAT79186
 ID AAT79186 standard; DNA; 32 BP.

XX
 AC AAT79186;
 XX
 DT 23-MAR-1998 (first entry)

XX Human full length CD40 antigen PCR primer.

XX Human; B7 antigen; CD40; PCR primer; monoclonal antibody; B cell; growth;
 KW differentiation; allergy; autoimmune disease; ss.
 XX
 OS Synthetic.

XX
 PN WO9731025-A1.
 XX
 PD 28-AUG-1997.

XX
 PF 21-FEB-1997; 97WO-US002858.
 XX
 PR 23-FEB-1996; 96US-00606293.

XX
 PA (CHIR) CHIRON CORP.
 XX
 PI De Boer M;

XX
 DR WPI; 1997-435094/40.
 XX

XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
 PT prevent their growth and differentiation, useful to treat or prevent
 PT antibody mediated allergies and autoimmune diseases.

XX Example 1; Fig 2; 64pp; English.

XX A novel humanised monoclonal antibody (MAB) has been developed which: (a)
 CC binds a human CD40 antigen on the surface of a B cell, to prevent its
 CC growth and differentiation; and (b) has an effective number of exposed
 CC amino acids in its framework regions that are consistent with amino acid
 CC residues found in the corresponding framework regions of a human Ab to
 CC provide a reduced immunogenicity in humans. The present sequence
 CC represent a PCR primer used in an example of the present invention. The
 CC MAB can be used to prevent or treat antibody mediated diseases,
 CC particularly immunoglobulin E (IgE) mediated allergies, systemic lupus
 CC erythematosus, primary biliary cirrhosis, idiopathic thrombocytopenia
 CC purpura and rheumatoid arthritis. The MAB inhibits the normal B cell
 CC response to CD40 ligands at relatively low concentrations and is unlikely
 CC to cause any immune response in humans

XX Sequence 32 BP; 4 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGGTCTCACCTCGCGCATGGTTTCG 55
 |||||
 Db 9 CTGGTCTCACCTCGCGCATGGTTTCG 32

RESULT 35
 AAQ55228/c
 ID AAQ55228 standard; DNA; 34 BP.

XX AC AAQ55228;
XX DT 25-MAR-2003 (revised)
XX DT 15-JUL-1994 (first entry)
XX DE Full length CD40 backward primer (MR112).
XX KW Antibody; monoclonal; membrane; transplant; rejection; sera; antigen;
XX KW graft-versus-host disease; auto-immune disease; allergy; cirrhosis;
XX KW idiopathic thrombocytopenic purpura; ss.
XX OS Synthetic.
XX PN WO9401547-A2.
XX PD 20-JAN-1994.
XX PF 08-JUL-1993; 93WO-US006432.
XX PR 09-JUL-1992; 92US-00910222.
XX PR 09-FEB-1993; 93US-00015147.
XX PR 28-MAY-1993; 93US-00070158.
XX PA (CETU) CETUS ONCOLOGY CORP.
XX PI De Boer M, Conroy LB;
XX PI WPI; 1994-035055/04.
XX DR Antibodies to membrane-associated antigens - used for treating transplant
XX PT rejection, graft-versus-host disease, antibody-mediated disease and auto-
XX PT immune disease.
XX PS Disclosure; Fig 2; 113pp; English.
XX CC Primers (AAQ55223-30) are used to amplify the human CD40 antigen and the
XX CC human B7 DNA. The CD40 antigen is immunoreactive with an anti- CD40 Mab.
XX CC The binding of the Mab to the CD40 antigen is located on the surface of a
XX CC human B cell. The antibodies can be used to treat transplant rejection
XX CC diseases as well as autoimmune infections. (Updated on 25-MAR-2003 to
XX CC correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 34 BP; 4 A; 12 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGTGG 905
DB 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 36
AAQ96202/c
ID AAQ96202 standard; DNA; 34 BP.
AC AAQ96202;
XX 26-MAR-1996 (first entry)
XX Primer #2.
XX Polymerase chain reaction; PCR; primer; amplify; B7; B-cell; T-cell;
XX KW baculovirus vector; hybridoma; antibody; antigen; immunosuppressor;
XX KW interleukin-2; IL-2; transplant rejection; graft vs host disease; GVHD;
XX KW rheumatoid arthritis; therapy; CD28; ss.
XX OS Synthetic.
XX PN WO9522619-A1.
XX PI De Boer M;
XX

PD 24-AUG-1995.
XX 19-JAN-1995; 95WO-US000897.
XX 18-FEB-1994; 94US-00200716.
XX PA (CETU) CETUS ONCOLOGY CORP.
XX PI De Boer M, Conroy LB;
XX PI WPI; 1995-302723/39.
XX DR T cell energy induction by coadmin. of anti-B7-antibody and
XX PT immunosuppressive agent - used to prevent transplant rejection, and to
XX PT treat graft vs host disease and rheumatoid arthritis.
XX PS Disclosure; p56; 77pp; English.
XX CC The sequences represented by AAQ96201-Q96204 are used in the invention.
XX CC The sequences represented by AAQ96197 and AAQ96198 are primers for the
XX CC full length B7-1. This sequence is also used (along with AAQ96200) as a
XX CC primer for soluble B7-1. This sequence corresponds to bases 307-324 of
XX CC the full length B7 gene. B7 is a monomeric transmembrane glycoprotein
XX CC that is expressed on activated B-cells, and is a ligand for the CD28
XX CC receptor of T-cells. There are three ligands of B7 (B7-1, B7-2, and B7-
XX CC 3). The sequence amplified by these primers is inserted into a
XX CC baculovirus vector and used for the production of B7-1 specific
XX CC antibodies using hybridoma techniques. The anti-B7-1 antibodies can then
XX CC be included in a composition containing an immunosuppressive agent that
XX CC inhibits the production of interleukin-2 (IL-2) by T-cells. This
XX CC composition can be administered to patients and thereby used to prevent
XX CC transplant rejection, and to treat graft vs host disease (GVHD) and
XX CC rheumatoid arthritis. The advantage with using this composition is that
XX CC it induces long-lasting T-cell anergy against an alloantigen
XX SQ Sequence 34 BP; 4 A; 12 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 882 GGCTGCACCCACCCAGGAGTGTGG 905
DB 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 37
AAAT79187/c
ID AAT79187 standard; DNA; 34 BP.
XX AAT79187;
XX 23-MAR-1998 (first entry)
XX Human full length CD40 antigen PCR primer.
XX DE Human; B7 antigen; CD40; PCR primer; monoclonal antibody; B cell; growth;
XX KW differentiation; allergy; autoimmune disease; ss.
XX OS Synthetic.
XX PN WO9731025-A1.
XX PD 28-AUG-1997.
XX PF 21-FEB-1997; 97WO-US002858.
XX PR 23-FEB-1996; 96US-00606293.
XX PA (CHIR) CHIRON CORP.
XX PI De Boer M;
XX

DR WPI; 1997-435094/40.
XX Humanised monoclonal antibody binding CD40 antigen on B cells - to
PT prevent their growth and differentiation, useful to treat or prevent
PT antibody mediated allergies and autoimmune diseases.
XX
XX Example 1; Fig 2; 64pp; English.
XX
XX A novel humanised monoclonal antibody (MAB) has been developed which: (a)
CC binds a human CD40 antigen on the surface of a B cell, to prevent its
CC growth and differentiation; and (b) has an effective number of exposed
CC amino acids in its framework regions that are consistent with amino acid
CC residues found in the corresponding framework regions of a human Ab to
CC provide a reduced immunogenicity in humans. The present sequence
CC represent a PCR primer used in an example of the present invention. The
CC MAB can be used to prevent or treat antibody mediated diseases,
CC particularly immunoglobulin E (IgE) mediated allergies, systemic lupus
CC erythematosus, primary biliary cirrhosis, idiopathic thrombocytopenia
CC purpura and rheumatoid arthritis. The MAB inhibits the normal B cell
CC response to CD40 ligands at relatively low concentrations and is unlikely
CC to cause any immune response in humans
XX
XX Sequence 34 BP; 4 A; 12 C; 12 G; 6 T; 0 U; 0 Other;
SQ Query Match 2.4%; Score 24; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 GGCTGCACCCACCCAGGAGTGTGG 905
Db 34 GGCTGCACCCACCCAGGAGTGTGG 11

RESULT 38
ADE28512
ID ADE28512 standard; DNA; 36 BP.
XX
XX ADE28512;
XX
XX 29-JAN-2004 (first entry)
XX
XX PCR primer SEQ ID 135 used to amplify human CD40 extracellular cDNA.
XX
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX human; PCR; primer; ss; extracellular domain.
XX
XX Homo sapiens.
XX
XX WO2003040170-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-US036107.
XX
XX 09-NOV-2001; 2001US-0348980P.
XX
XX (PFIZ) PFIZER PROD INC.
XX (ABGE-) ABGENIX INC.
XX
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX WPI; 2003-441521/41.
XX
XX New chimeric or human monoclonal antibody or its antigen-binding portion
XX that specifically binds to and activates human CD40, useful for enhancing
XX an immune response in a human, or treating cancer, HIV, neutropenia or
XX viral infections.
XX
XX Example 14; SEQ ID NO 135; 177pp; English.
XX
XX The invention relates to a novel chimeric or human monoclonal antibody or

CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody-related PCR primer of the invention.
XX
SQ Sequence 36 BP; 6 A; 11 C; 9 G; 10 T; 0 U; 0 Other;
Query Match 2.3%; Score 23.4; DB 10; Length 36;
Best Local Similarity 96.0%; Pred. No. 1.4e+04;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 46 CCATGGTTCGTCCTGCTGCAGTG 70
Db 12 CAATGGTTCGTCCTGCTGCAGTG 36

RESULT 39
AAZ40937
ID AAZ40937 standard; DNA; 23 BP.
XX
XX AAZ40937;
XX
XX 26-JAN-2000 (first entry)
XX
XX Human CD40 PCR forward primer SEQ ID NO:86.
XX
XX Identification; genetic target; gene modulation; human; probe;
XX antisense oligonucleotide; phosphorothioate; PCR primer;
XX nucleotide sequence-based technology; antisense drug discovery;
XX target validation; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9953101-A1.
XX
XX 21-OCT-1999.
XX
XX 13-APR-1999; 99WO-US008268.
XX
XX 13-APR-1998; 98US-0081483P.
XX
XX 28-APR-1998; 98US-00067638.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM, Baker BF, McNeill J, Freier SM, Saamur HM, Brooks DG;
XX Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
XX WPI; 1999-620446/53.
XX
XX Identifying compounds which modulate expression of nucleic acids, used to
XX provide compounds having defined physical, chemical or bioactive
XX properties, e.g. antisense activity.
XX
XX Example 10; Page 84; 264pp; English.
XX
XX A method has been developed of defining a set of compounds that modulate
XX the expression of a target nucleic acid (tNA) sequence via binding of the
XX compounds with the tNA sequence. The method comprises generating a
XX library of virtual compounds in silico according to defined criteria, and
XX evaluating in silico the binding of the virtual compounds with the tNA
XX according to defined criteria. Also described are: (1) a method of
XX defining a set of oligonucleotides (ONs) that modulate the expression of
XX a tNA sequence via binding of the ONs with the tNA sequence comprising
XX generating a library of virtual compounds in silico according to defined
XX criteria, and evaluating in silico the binding of the virtual ONs with
XX the tNA according to defined criteria; and (2) a method of defining a set

CC of compounds that modulate the expression of a tNA sequence via binding
CC and identification of synthetic compounds having defined physical,
CC chemical or bioactive properties. Information gathered from assays of
CC such compounds is used to identify nucleic acid sequences that are
CC tractable to a variety of nucleotide sequence-based technologies, e.g.
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
CC AA52701 to AA52706, represent sequences used in the exemplification of
CC the present invention

XX SQ Sequence 23 BP; 8 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.3%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 CAGAGTTCACGAAACGGAATGC 224
|||||
Db 1 CAGAGTTCACGAAACGGAATGC 23

RESULT 40
AAZ40938/c
ID AAZ40938 standard; DNA; 23 BP.

XX AC AAZ40938;

XX DT 26-JAN-2000 (first entry)

XX DE Human CD40 PCR reverse primer SEQ ID NO:87.

XX KW Identification; Genetic target; gene modulation; human; probe;
XX KW antisense oligonucleotide; phosphorothioate; PCR primer;
XX KW nucleotide sequence-based technology; antisense drug discovery;
XX KW target validation; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09953101-A1.

XX PD 21-OCT-1999.

XX PF 13-APR-1999; 99WO-US008268.

XX PR 13-APR-1998; 98US-0081493P.

XX PR 28-APR-1998; 98US-00067638.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Cowser LM, Baker BF, Mcneil J, Freier SM, Sasnor HM, Brooks DG;

XX PI Chasi C, Wyatt JR, Borchers AH, Vickers TA;

XX DR WPI; 1999-620446/53.

XX PT Identifying compounds which modulate expression of nucleic acids, used to
XX PT provide compounds having defined physical, chemical or bioactive
XX PT properties, e.g. antisense activity.

XX PS Example 10; Page 84; 264pp; English.

XX CC A method has been developed of defining a set of compounds that modulate
XX CC the expression of a target nucleic acid (tNA) sequence via binding of the
XX CC compounds with the tNA sequence. The method comprises generating a
XX CC library of virtual compounds in silico according to defined criteria, and
XX CC evaluating in silico the binding of the virtual compounds with the tNA
XX CC according to defined criteria. Also described are: (1) a method of
XX CC defining a set of oligonucleotides (ONs) that modulate the expression of
XX CC a tNA sequence via binding of the ONs with the tNA sequence comprising
XX CC generating a library of virtual compounds in silico according to defined
XX CC criteria, and evaluating in silico the binding of the virtual ONs with
XX CC the tNA according to defined criteria; and (2) a method of defining a set
XX CC of compounds that modulate the expression of a tNA sequence via binding

CC of the compounds with the tNA. The methods can be used for the generation
CC and identification of synthetic compounds having defined physical,
CC chemical or bioactive properties. Information gathered from assays of
CC such compounds is used to identify nucleic acid sequences that are
CC tractable to a variety of nucleotide sequence-based technologies, e.g.
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
CC AA52701 to AA52706, represent sequences used in the exemplification of
CC the present invention

XX SQ Sequence 23 BP; 1 A; 5 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 2.3%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 GAACAGAGAGACACACTGCCACC 282
|||||
Db 23 GAACAGAGAGACACACTGCCACC 1

RESULT 41

AAZ47771/c

ID AAZ47771 standard; DNA; 23 BP.

XX AC AAZ47771;

XX DT 02-MAR-2000 (first entry)

XX DE Human CD40 reverse PCR primer SEQ ID NO:87.

XX KW Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
XX KW expression; immune disease; inflammatory disease; immunomodulatory;
XX KW anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;
XX KW anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;
XX KW hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
XX KW inflammatory bowel disease; asthma; psoriasis; cancer; tumour;
XX KW PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09957320-A1.

XX PD 11-NOV-1999.

XX PF 22-APR-1999; 99WO-US008765.

XX PR 01-MAY-1998; 98US-00071433.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Cowser LM;

XX DR WPI; 2000-062158/05.

XX PT Antisense molecules directed against nucleic acid encoding human CD40,
XX PT for treating e.g. immune, inflammatory or hyperproliferative diseases.

XX PS Example 13; Page 50; 102pp; English.

XX CC AAZ47685 to AAZ47768 represent phosphorothioate antisense
XX CC oligonucleotides targeted to human CD40, which can be used to inhibit the
XX CC expression of human CD40. CD40 is involved in lymphocyte activation,
XX CC tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
XX CC prevent immune-associated diseases (specifically guest vs. host disease,
XX CC allograft rejection or autoimmune diseases); inflammation (specifically
XX CC asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
XX CC disease or psoriasis) or hyperproliferation (specifically cancer and
XX CC tumours). the antisense oligonucleotides are also useful as diagnostic
XX CC and research reagents. AAZ47769 represents the human CD40 nucleotide
XX CC sequence. AAZ47770 to AAZ47772 represent human CD40 forward and reverse
XX CC PCR primers, and a human CD40 PCR probe, respectively. AAZ47773 to
XX CC AAZ47775 represent other PCR primers and a probe used in the

```
CC exemplification of the present invention
XX
SQ Sequence 23 BP; 1 A; 5 C; 8 G; 9 T; 0 U; 0 Other;

Query Match      2.3%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 GAACAGAGAGACACACTGCCACC 282
DB 23 GAACAGAGAGACACACTGCCACC 1

RESULT 42
AAZ47770
ID AAZ47770 standard; DNA; 23 BP.
AC AAZ47770;
XX
DT 02-MAR-2000 (first entry)
XX
DE Human CD40 forward PCR primer SEQ ID NO:86.
XX
KW Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
KW expression; immune disease; inflammatory disease; immunomodulatory;
KW anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;
KW anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;
KW hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
KW inflammatory bowel disease; asthma; psoriasis; cancer; tumour;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO957320-A1.
XX
PD 11-NOV-1999.
XX
PF 22-APR-1999; 99WO-US008765.
XX
PR 01-MAY-1998; 98US-00071433.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CP, Cowser LM;
XX
WI WPI; 2000-062158/05.
XX
PT Antisense molecules directed against nucleic acid encoding human CD40,
XX for treating e.g. immune, inflammatory or hyperproliferative diseases.
XX
PS Example 13; Page 50; 102pp; English.
XX
CC AAZ47685 to AAZ47768 represent phosphorothioate antisense
CC oligonucleotides targeted to human CD40, which can be used to inhibit the
CC expression of human CD40. CD40 is involved in lymphocyte activation,
CC tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
CC prevent immune-associated diseases (specifically guest vs. host disease,
CC allograft rejection or autoimmune diseases); inflammation (specifically
CC asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
CC disease or psoriasis) or hyperproliferation (specifically cancer and
CC tumours). the antisense oligonucleotides are also useful as diagnostic
CC and research reagents. AAZ47769 represents the human CD40 nucleotide
CC sequence. AAZ47770 to AAZ47772 represent human CD40 forward and reverse
CC PCR primers, and a human CD40 PCR probe, respectively. AAZ47773 to
CC AAZ47775 represent other PCR primers and a probe used in the
CC exemplification of the present invention
XX
SQ Sequence 23 BP; 8 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      2.3%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 CAGAGTTCACTGAAACGGAATGC 224
DB 1 CAGAGTTCACTGAAACGGAATGC 23

RESULT 43
ACH66633
ID ACH66633 standard; DNA; 23 BP.
XX
AC ACH66633;
XX
DT 06-NOV-2003 (first entry)
XX
DE Real-time PCR probe used to detect human CD40 expression.
XX
KW Human; ss; PCR; probe; real-time PCR; costimulatory molecule; CD40;
KW major histocompatibility complex; MHC; class I; class II; antigen;
KW tumour; deacetylase inhibitor; DAI; tumourogenesis; immune system;
KW T lymphocyte; T cell activation; immunogenicity; antigen presentation;
KW cell lysis; trichostatin A; TSA; sodium butyrate; cytostatic; CD40.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= 5' terminal 6-carboxyfluorescein (FAM) "
FT modified_base 23 /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= 3' terminal N,N,N'-tetramethyl-6-
FT carboxyrhodamine (TAMRA) "
XX
PN US6518012-B1.
XX
PD 11-FEB-2003.
XX
PF 31-MAR-2000; 2000US-00540257.
XX
PR 02-APR-1999; 99US-0127591P.
XX 29-JUL-1999; 99US-0146275P.
XX (HEAL-) HEALTH RES INC.
XX
PI Tomasi TB;
XX
WI WPI; 2003-575859/54.
XX
PT Increasing expression of gene in tumor cells in vitro comprises
XX contacting tumor cells with deacetylase inhibitor.
XX
PS Example 1; Fig 9; 20pp; English.
XX
CC The invention discloses a method for increasing the expression of
CC costimulatory molecules, such as CD40, and major histocompatibility
CC complex (MHC) class I and class II antigens in tumour cells in vitro. The
CC method comprises contacting the tumour cells with deacetylase inhibitor
CC (DAI). Tumourogenesis is related, in part, to the failure of the immune
CC system to reject spontaneously arising tumours by responding
CC appropriately to tumour antigens. Induction of T lymphocytes is
CC considered to be a critical initial step and T cell activation requires
CC an antigen specific signal, which involves the antigenic peptide and the
CC MHC class I and II proteins. The increased expression of these molecules
CC increases the immunogenicity of tumours and their susceptibility to
CC lysis. The inhibitors of deacetylation, at low concentrations, produce
CC little or no apoptosis and maintain a normal cell cycle. The expression
CC of MHC genes, and other molecules of immunologic importance, in antigen
CC presentation and cell lysis on cells is induced. The DAIs are preferably
CC trichostatin A (TSA) or sodium butyrate. The sequence presented is a real
CC -time PCR probe used to detect expression levels of the human CD40 gene
```

```
XX SQ Sequence 23 BP; 1 A; 8 C; 7 G; 7 T; 0 U; 0 Other;
Query Match      2.3%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 58 TGCCTCTGCAGTGGCTCTCTGG 80
Db 1 TGCCTCTGCAGTGGCTCTCTGG 23

RESULT 44
ID ADY75648/c
XX ADY75648 standard; DNA; 23 BP.
AC ADY75648;
XX
DT 02-JUN-2005 (first entry)
XX Human CD40 reverse RT-PCR primer.
XX
KW RT-PCR; primer; ss; diagnosis; drug discovery; mass spectroscopy;
KW reverse transcriptase PCR; CD40.
XX
OS Homo sapiens.
XX
PN WO2005023986-A2.
XX
PD 17-MAR-2005.
XX
PF 07-SEP-2004; 2004WO-US028879.
XX
PR 04-SEP-2003; 2003US-0500723P.
PR 04-SEP-2003; 2003US-0500724P.
PR 04-SEP-2003; 2003US-0500730P.
PR 04-SEP-2003; 2003US-0500732P.
PR 04-SEP-2003; 2003US-0500824P.
PR 11-SEP-2003; 2003US-0502007P.
PR 11-SEP-2003; 2003US-0502076P.
PR 17-SEP-2003; 2003US-0504495P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Griffey RH, Bennett CF, Ecker DJ, Ward DT, Freier SM;
XX
XX WPI; 2005-233282/24.
XX
XX Selecting a target molecule having affinity for a ligand that is equal
XX to/greater than a baseline affinity by introducing a target molecule into
XX a ligand and standard target test mixture and identifying complex by mass
XX spectrometer.
XX
XX Example 65; SEQ ID NO 153; 314pp; English.
XX
XX The invention relates to selecting a target molecule that has an affinity
XX for a ligand that is equal to or greater than a baseline affinity, ligand
XX comprises introducing a target molecule into a test mixture of the ligand
XX and a standard target, introducing the test mixture into a mass
XX spectrometer and identifying any complexes of the target molecule and the
XX ligand. Also included are a method of detecting a ligand-target complex
XX having an affinity as expressed as a dissociation constant of nanomolar-
XX 100 millimolar, a method for determining the relative interaction between
XX at least two molecules determining target a ligand, a method of
XX determining binding interaction (between a first target molecule and a
XX second target molecule with respect to a ligand), a method of determining
XX the relative proximity of binding sites for a first target molecule and a
XX second target molecule on a ligand, a method of determining the relative
XX orientation of a first target molecule to a second target molecule when
XX bound to a ligand, a method for screening target molecules having binding
XX affinity to a ligand, a method for modulating the binding affinity of a
XX target molecule for a ligand, a method for refining the binding of a
XX target molecule to a ligand, a method of favoring an alternate structure
```

```
CC of an oligomer, a method for identifying a ligand that alters a target
CC compound secondary structure, a method of determining the relative change
CC in proximity of binding sites for a first ligand and a second ligand on a
CC target substrate influenced by the first ligand, a method of determining
CC the relative change in proximity of a first binding site for a binding
CC ligand and a second binding site for a second binding ligand on a target,
CC a method of determining the relative orientation of a first ligand to a
CC second ligand when bound to a target substrate, an oligomeric compound
CC comprising a nucleotide sequence at least 80% complementary to a target
CC RNA (where the oligomeric compound comprises 21-24 nucleotides, and
CC comprises a nucleotide sequence that corresponds to a portion of the
CC nucleotide sequence of a larger oligomeric compound that comprises a
CC stemloop structure), a method of modulating transcription in a cell, a
CC method of modulating translation in a cell, a method of modulating a
CC conversion of a precursor RNA into a microRNA in a cell, a method of
CC generating a set of (oligomeric) compounds that modulate the expression
CC of a target nucleic acid molecule, a computer formatted medium comprising
CC computer readable instructions for identifying active compounds or for
CC performing the method above, a method of predicting evolutionarily
CC allowed mutations of a microRNA, a method of grouping biological members
CC according to a grouping criteria, a method of determining a blur-factor
CC and a method of determining a group of probable mutations for a microRNA.
CC The methods of the invention may be applied to the design of siRNA (short
CC interfering RNA) and antisense oligonucleotides. The method is useful for
CC determining the mode of binding interaction between two or more target
CC molecules to the ligand as well as their relative affinities. The
CC oligomeric compounds are useful in drug discovery and target validation,
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence is an RT-PCR (reverse transcriptase PCR) primer for
CC human CD40 mRNA used to assess expression of CD40 during treatment with
CC antisense oligonucleotides targeted to the human CD40 gene, designed
CC according to the methods of the invention.
XX
```

SQ Sequence 23 BP; 1 A; 5 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 2.3%; Score 23; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 260 GAACAGAGAGACACACTGCCACC 282

Db 23 GAACAGAGAGACACACTGCCACC 1

RESULT 45

ADY75647

ID ADY75647 standard; DNA; 23 BP.

XX AC ADY75647;

XX

DT 02-JUN-2005 (first entry)

XX

DE Human CD40 forward RT-PCR primer.

XX

KW RT-PCR; primer; ss; diagnosis; drug discovery; mass spectroscopy;

KW reverse transcriptase PCR; CD40.

XX

OS Homo sapiens.

XX

PN WO2005023986-A2.

XX

PD 17-MAR-2005.

XX

PF 07-SEP-2004; 2004WO-US028879.

XX

PR 04-SEP-2003; 2003US-0500723P.

PR

PR 04-SEP-2003; 2003US-0500724P.

PR

PR 04-SEP-2003; 2003US-0500730P.

PR

PR 04-SEP-2003; 2003US-0500732P.

PR

PR 04-SEP-2003; 2003US-0500824P.

PR

PR 11-SEP-2003; 2003US-0502007P.

PR

PR 11-SEP-2003; 2003US-0502076P.

PR

PR 17-SEP-2003; 2003US-0504495P.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 08:52:01 ; Search time 3986 Seconds
(without alignments)
11784.805 Million cell updates/sec

Title: US-10-698-689-85
Perfect score: 1004
Sequence: 1 gctcgctcgccgcccagt.....ccagtcagtcgagccctc 1004

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hic:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_ges1:
10: gb_ges2:
11: gb_ges3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	5.0	50	1	AU107930
2	48.4	4.8	50	1	AU107931
3	46.4	4.6	49	8	H94398
4	40	4.0	50	1	AU107932
5	38.8	3.9	48	8	H95733
6	22.8	2.3	34	1	A1431428
7	21.8	2.2	49	10	CG732711
8	21	2.1	50	1	AU106947
9	20.6	2.1	43	1	A1440496
10	20.6	2.1	46	1	A1250491
11	20.6	2.1	46	1	A1582504
12	20.6	2.1	50	1	AU106810
13	20.4	2.0	40	1	A1678633
14	20.4	2.0	46	10	CZ265995
15	20.4	2.0	48	1	AA399365
16	20.2	2.0	49	9	BH759224
17	20.2	2.0	50	1	AU107338
18	20	2.0	45	2	BE393504
19	19.8	2.0	50	1	AU102718
20	19.8	2.0	50	1	AU104759
21	19.8	2.0	50	1	AU104763
22	19.6	2.0	41	9	AZ449036

```
c 96 18.2 1.8 47 9 AZ805275 2M0066P01
c 97 18.2 1.8 48 9 AZ993115 2M0278G04
c 98 18.2 1.8 49 1 AI001175 ov19a12.8
c 99 18.2 1.8 49 1 AA122130 zn82f09.r
c 100 18.2 1.8 50 1 AA798983 vv95f06.r
c 101 18.2 1.8 50 1 AU102452 AU102452
c 102 18.2 1.8 50 1 AU104124 AU104124
c 103 18.2 1.8 50 1 AU104940 AU104940
c 104 18.2 1.8 50 1 AU104943 AU104943
c 105 18.2 1.8 50 1 AU105236 AU105236
c 106 18.2 1.8 50 1 AU106428 AU106428
c 107 18.2 1.8 50 1 AU106860 AU106860
c 108 18.2 1.8 50 1 AU107339 AU107339
c 109 18.2 1.8 50 6 CB410572 NISC nc12
c 110 18 1.8 29 8 DN955450 it87h12.g
c 111 18 1.8 42 9 CC326042 RS7753.Ba
c 112 18 1.8 43 10 CZ477690 dl1365-3p
c 113 18 1.8 45 5 BX621624 BX621624
c 114 18 1.8 46 3 BI488502 603021011
c 115 18 1.8 48 1 AV845590 AV845590
c 116 18 1.8 48 6 CA965843 CCLX05a19
c 117 18 1.8 49 1 AA934654 oo7le06.s
c 118 18 1.8 49 9 CC887819 SALK 1508
c 119 18 1.8 50 1 AU102653 AU102653
c 120 18 1.8 50 1 AU103142 AU103142
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ALIGNMENTS

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RESULT 1
AU107930 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU107930 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC00913, mRNA sequence.
ACCESSION AU107930.1 GI:13557452
VERSION AU107930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tanoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
TITLE mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
Location/Qualifiers
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN

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Query Match 5.0%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 18 AGTGGTCTGCGCGCTGGTCTTACCTCGCCATGGTTCGCTGCTGCTGCA 67
|||||
Db 1 AGTGGTCTGCGCGCTGGTCTTACCTCGCCATGGTTCGCTGCTGCTGCA 50
|||||

RESULT 2
AU107931 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU107931 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC02683, mRNA sequence.
ACCESSION AU107931.1 GI:13557453
VERSION AU107931
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tanoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
TITLE mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
Location/Qualifiers
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN

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Query Match 4.8%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 0.044;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 23 TCCTGCGCGCTGGTCTTACCTCGCCATGGTTCGCTGCTGCTGCGG 72
|||||
Db 1 TCCTGCGCGCTGGTCTTACCTCGCCATGGTTCGCTGCTGCTGCGG 50
|||||
```

RESULT 3

```
H94398
LOCUS H94398 49 bp mRNA linear EST 25-NOV-1996
DEFINITION Yv17809.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:243016 5' similar to gb:X60592 CD40L RECEPTOR PRECURSOR
(HUMAN); contains 11 repetitive element ;, mRNA sequence.
ACCESSION H94398.1 GI:1102031
VERSION H94398
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
```


double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo."

ORIGIN

Query Match 3.9%; Score 38.8; DB 8; Length 48;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 770 TCTTCTGGTCCCAACTGCTGCTCCAGTGCAGAGACTTTACATGG 817
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 TCTTCTGGATCCANACTGCTGCTNCAGTCCAGGAGACTTTANATGG 48
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6

AI431428

LOCUS AI431428 34 bp mRNA linear EST 30-MAR-1999
DEFINITION th36g09.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2120416 3'
similar to TR:Q04117 Q04117 SALIVARY PROLINE-RICH PROTEIN RP4
PRECURSOR. ;contains element MSR1 repetitive element ;, mRNA
sequence.

ACCESSION

VERSION AI431428.1 GI:4303117

KEYWORDS

EST.

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

1 (bases 1 to 34)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 917 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 1.

FEATURES

source

1..34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2120416"
/tissue_type="adenocarcinoma"
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/clone_lib="NCI CGAP Panl"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: SalI;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN

Query Match 2.3%; Score 22.8; DB 1; Length 34;
Best Local Similarity 79.4%; Pred. No. 4.3e+05;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 703 CCAGAAGCCCAACCAATAAGGCCCCCAACCCCA 736
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 CCAAAAACCAAAAAAAGGGCCCCCAACCCCA 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7

CG732711/c

LOCUS

CG732711 49 bp DNA linear GSS 20-OCT-2003
1119150E01.1BL.x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.

ACCESSION

CG732711 GI:37775203

KEYWORDS

GSS.

SOURCE

ORGANISM Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 49)

Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon

TITLE

Unpublished (2001)

JOURNAL

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1119150 row: 46

Class: transposon-tagged.

Location/Qualifiers

1..49

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1119 - RescueMu Grid AA"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site.1: BamHI, Site.2: BglII;

RescueMu is a 4.9 Kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA

was extracted from leaf strips, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

plates with ampicillin."

ORIGIN

Query Match 2.2%; Score 21.8; DB 10; Length 49;
Best Local Similarity 70.7%; Pred. No. 9.1e+05;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 629 CCTGTGGTGATCCCATCATCTTCGGGATCCTGTTGCCA 669
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 41 CCTGTTCCAGCTCAACGTCCATCGGATCCTGTTGCCA 1
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8

AU106947/c

LOCUS

AU106947 50 bp mRNA linear EST 28-JAN-2004
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cdna clone
ZRV6C565, mRNA sequence.

ACCESSION

AU106947

VERSION

AU106947.1 GI:13556468

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

```

REFERENCE
AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,I., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
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/mol_type="mRNA"
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/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
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Best Local Similarity 73.0%; Pred. No. 1.5e+06;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 781 CCAACACGTGCTCCAGTCGAGGAGACTTTACATGG 817
||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 50 CCAACGCTGCTCCACAGACCCAGAGGCTTAAATGG 14

RESULT 9
AI440496 43 bp mRNA linear EST 18-MAR-1999
LOCUS tc88h12.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2073287 3'
DEFINITION similar to TR:Q04118 Q04118 SALIVARY PROLINE-RICH GLYCOPROTEIN G1
PRECURSOR. ; contains MER22.t1 MSR1 repetitive element ;, mRNA
sequence.
ACCESSION AI440496
VERSION AI440496.1 GI:4300635
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 505 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
source Location/Qualifiers
1..43
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2073287"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/clone_lib="NCI CGAP CLL1"
/notes="Vector: p773B-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15',
TGTTACCAATCTGAAGTGGAGCGCGCATGCTTTTTCCTTTTTCCTTTT
T 3'; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 2.1%; Score 20.6; DB 1; Length 43;
Best Local Similarity 74.3%; Pred. No. 1.9e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 707 GAAGCCCAACCAATAGGCCCCACCCCAAGCAGG 741
||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8 GAAAAAAGAAAAAGGCCCCCAAGCAGG 42

RESULT 10
AI250491 46 bp mRNA linear EST 21-DEC-1998
LOCUS qx27h02.x1 NCI CGAP Ov34 Homo sapiens cDNA clone IMAGE:2002611 3'
DEFINITION similar to gb:L21696 cds1 PROTHYMOSIN ALPHA (HUMAN); contains
element MER25 repetitive element ;, mRNA sequence.
ACCESSION AI250491
VERSION AI250491.1 GI:3847020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 404 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
source Location/Qualifiers
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2002611"
/sex="female"
/tissue_type="borderline ovarian carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ov34"
/notes="Organ: ovary; Vector: pAMP1; mRNA made from
borderline ovarian carcinoma, cDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 500 bp. Primary library,
non-amplified."

ORIGIN
Query Match 2.1%; Score 20.6; DB 1; Length 46;
Best Local Similarity 74.3%; Pred. No. 1.9e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

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Qy 634 TGGTGATCCCATCATCTTCGGGATCCCTGTTGCC 668
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 42 TGGTCATCCTCATCATCTTCAGCTGCCCGCGTGCC 8

RESULT 11
A1582504
LOCUS
DEFINITION
ts01905.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2227352 3'
similar to SW:PRPL_HUMAN F10162 SALIVARY PROLINE-RICH PROTEIN PO ;,
mRNA sequence.
A1582504
A1582504.1 GI:4568401
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1924 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES
source
1..46
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2227352"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Pan1"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 2.1%; Score 20.6; DB 1; Length 46;
Best Local Similarity 67.4%; Pred. No. 1.9e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 693 AAAAAGTGGCCAGAGCCCAACCAATAAGCCCCCCCCCA 735
||||| ||||| ||||| ||||| ||||| |||||
Db 4 AAAAAGGGGGCAAAAAAAGGGGGCCCCCCCCCCCCCA 46

RESULT 12
A106810
LOCUS
DEFINITION
A106810 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS03581, mRNA sequence.
A106810
A106810.1 GI:13556331
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1290 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

```

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS03581"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.1%; Score 20.6; DB 1; Length 50;
Best Local Similarity 67.4%; Pred. No. 2e+06;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 934 AGAGCCTGGTGCTGCTGCAGGGTGCAGGCAGAGCGGGG 976
||||| ||||| ||||| ||||| ||||| |||||
Db 7 AGAGCCTAGTCGCGTGTGGAGAGGTATCGCGCGGGCAGGG 49

RESULT 13
A1678633
LOCUS
DEFINITION
tu84h12.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2257799 3'
similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15
PRECURSOR. ; contains element MSR1 repetitive element ;, mRNA
sequence.
A1678633
A1678633.1 GI:4888815
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1290 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

```

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source
1. 40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2257799"
/tissue_type="poorly differentiated adenocarcinoma with
signal ring cell features"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Gas4"
/notes="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN
Query Match 2.0%; Score 20.4; DB 1; Length 40;
Best Local Similarity 71.1%; Pred. No. 2.1e+06;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 698 GGTGCCCAAGACCAACCAATAAGGCCGCCGCCACCCCA 735
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 GGGGGGAAGAAAAAACCACCAAAACCCGCCGCCCA 40

RESULT 14
LOCUS C2265995 46 bp mRNA linear GSS 11-APR-2005
DEFINITION CB0052 Sanger Institute Gene Trap Library pGT01xft2v Mus musculus
cDNA, mRNA sequence.
ACCESSION C2265995
VERSION C2265995.1 GI:60393817
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 46)
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1373 Std Error: 0.00
Seg primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 46
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/strain="129 OLA"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xft2v"
/notes="Vector: pGT01xft2v"

ORIGIN
Query Match 2.0%; Score 20.4; DB 10; Length 46;
Best Local Similarity 65.2%; Pred. No. 2.2e+06;
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 647 CATCTTCGGGATCTCTTTGTCATCTCTTGGTCTGCTTTATC 692
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 46 CTTTCATCAGCCTCTGCTGTCGCCGCCATCTTGGATCTGGTGTGCTC 1

RESULT 15
LOCUS AA399365 49 bp DNA linear GSS 12-MAR-2002
DEFINITION KG00450-3prime Drosophila melanogaster P{SUPor-p} P element
insertion lines Drosophila melanogaster genomic sequence recovered
from 3' end of P element, genomic survey sequence.

```

```

LOCUS AA399365 48 bp mRNA linear EST 08-AUG-1997
DEFINITION zt50d07.s1 Soares ovary tumor NBOT Homo sapiens cDNA clone
IMAGE:725773 3' similar to WP:C54G4.1 CE05507 RIBOSOMAL S6 KINASE
; mRNA sequence.
ACCESSION AA399365
VERSION AA399365.1 GI:2053171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 48)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1373 Std Error: 0.00
Seg primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 48
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5937717"
/db_xref="taxon:9606"
/clone="IMAGE:725773"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NBOT"
/notes="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

ORIGIN
Query Match 2.0%; Score 20.4; DB 1; Length 48;
Best Local Similarity 71.1%; Pred. No. 2.2e+06;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 938 CCTGTGCTGCTGCTGCGGGGTGTCAGGCGAGCGGG 975
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 41 CCTGTCTCTGAGCTGCTGCGGGCGGGAGCTGCTG 4

RESULT 16
LOCUS BH759224 49 bp DNA linear GSS 12-MAR-2002
DEFINITION KG00450-3prime Drosophila melanogaster P{SUPor-p} P element
insertion lines Drosophila melanogaster genomic sequence recovered
from 3' end of P element, genomic survey sequence.

```

```
ACCESSION BH759224
VERSION BH759224.1 GI:19352463
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 49)
REFERENCE
AUTHORS Lewis,R., Hoskins,R., Liao,G., Mozden,N., Tsang,G., He,Y.,
Karpén,G., Bellen,H., Rubin,G. and Spradling,A.
TITLE The Berkeley Drosophila Genome Project Gene Disruption Project
JOURNAL Unpublished (2001)
COMMENT Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5108439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 1 in the 49 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
FEATURES
source
Location/Qualifiers
1..49
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P{SUPor-P} P element
insertion lines"
/notes="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P{SUPor-P} P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."
```

ORIGIN

Query Match 2.0%; Score 20.2; DB 9; Length 49;
Best Local Similarity 75.8%; Pred. No. 2.5e+06;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 767 CGATCTCTGGCTCCCAACTGCTGCTCCAGT 799

Db 43 CGCTCTTTGGGGTCCCAAAACCGTGTCCATT 11

RESULT 17

AU107338
LOCUS AU107338 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION CAS04142, mRNA sequence.
VERSION AU107338.1 GI:13556859

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Suzuki,Y., Iaira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

PUBMED 11375929
COMMENT Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES

source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS04142"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 2.0%; Score 20.2; DB 1; Length 50;
Best Local Similarity 68.3%; Pred. No. 2.5e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 758 TTTTCCGACGATCTTCCTGGCTCCACACTGCTGCTCCAG 798

Db 3 TATCTCGATGCGCTTTCTCGGCGACATCTCTGCTCTCG 43

RESULT 18

BE393504
LOCUS BE393504 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3632638 5',
DEFINITION mRNA sequence.
ACCESSION BE393504
VERSION BE393504.1 GI:9338869

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 45)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM324 row: e column: 23
High quality sequence stop: 45.

FEATURES

source
Location/Qualifiers
1..45
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3632638"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 44"

/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 2.0%; Score 20; DB 2; Length 45;

Best Local Similarity 72.2%; Pred. No. 2.8e+06;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 170 CCAGCCAGCAGACAACTGGTGCAGTCACTGCACAGA 205
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 4 CCAGCAAGCAGCAGCAGCAGCAGTTCAGCCAGTTCACAGA 39

RESULT 19
AUI02718/c
LOCUS AUI02718.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI02718 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT06130, mRNA sequence.
ACCESSION AUI02718
VERSION AUI02718.1 GI:13552239
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT06130"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 77.4%; Pred. No. 3.2e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 879 TGAGGCTGCACCCACCCAGGAGTGTGGCCAC 909
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 31 TGAGGCTGCAGCCCTCTCTGGGTGAGGGCAC 1

RESULT 21
AUI04763/c
LOCUS AUI04763.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI04763 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HST01164, mRNA sequence.
ACCESSION AUI04763
VERSION AUI04763.1 GI:13554284
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT06130"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 63.8%; Pred. No. 3.2e+06;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 305 CCTAGGGCTTCGGTCCAGCAGAGCGCAGCTTCAGAAACAGACCA 351
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 48 CCCATGGCAGCGGTCCAGTTCACAGCGCGGCCGGAAGAGGAACA 2

RESULT 20
AUI04759/c
LOCUS AUI04759.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI04759 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS10241, mRNA sequence.
ACCESSION AUI04759
VERSION AUI04759.1 GI:13554280
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS10241"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 77.4%; Pred. No. 3.2e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 879 TGAGGCTGCACCCACCCAGGAGTGTGGCCAC 909
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 31 TGAGGCTGCAGCCCTCTCTGGGTGAGGGCAC 1

RESULT 21
AUI04763/c
LOCUS AUI04763.1 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AUI04763 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HST01164, mRNA sequence.
ACCESSION AUI04763
VERSION AUI04763.1 GI:13554284
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HST01164"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.8; DB 1; Length 50;
Best Local Similarity 77.4%; Pred. No. 3.2e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      879  TGAGGCTGACCCACCCAGGAGTGTGGCCAC 909
      |||||
Db      31  TGAGGCTGACCGCGCTCTGGGGTGAGGGCAC 1

RESULT 22
A2449036/c
LOCUS   A2449036           41 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION clone UUGC1M0247P02 F, genomic survey sequence.
ACCESSION A2449036
VERSION   A2449036.1 GI:10602425
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weisse,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
COMMENT   University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: dunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0247 row: P column: 02
          Seq primer: CGTTGTAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 41.

FEATURES             Location/Qualifiers
     source           1..41
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0247P02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
          musculus C57BL/6J (male) was obtained from the Jackson
          Laboratory Mouse DNA Resource
          (http://www.jax.org/resources/documents/dnares/). The DNA
          was hydrodynamically sheared by repeated passage through a
          0.005 inch orifice at constant velocity. The sheared DNA
          was blunt end-repaired with T4 DNA polymerase and T4
          polynucleotide kinase. Adaptor oligonucleotides were
          ligated to the blunt ends in high molar excess. The
          adaptor DNA was purified and size-selected for a 9.5 to
          10.5 kb range using preparative agarose gel
          electrophoresis. Vector DNA was prepared from a derivative
          of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
          inducible derivative of plasmid R1. The vector was ligated
          with adaptors complementary to the insert adaptors and
          purified. The sheared, adaptor mouse DNA was annealed to
          adaptor vector DNA, and transformed into
          chemically-competent E. coli XL10-Gold (Stratagene) cells
          and selected for ampicillin resistance."

ORIGIN
Query Match      2.0%; Score 19.6; DB 9; Length 41;
Best Local Similarity 73.5%; Pred. No. 3.5e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      398  GAGCTGTGTCTGCACCGCTCATGCTCGCCCGCTTGGGGT 439
      |||||
Db      1  GCCTCGCCCTCGCCCTCTCTCCGCCCGCTCCCGGT 42

RESULT 24
AUI04419/c
LOCUS   AUI04419          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AUI04419 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
          HEP22703, mRNA sequence.
ACCESSION AUI04419
VERSION   AUI04419.1 GI:13553940
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
          EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL   Contact: Yutaka Suzuki
COMMENT   Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="COLF1717"
                     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      2.0%; Score 19.6; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.7e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      398  GAGCTGTGTCTGCACCGCTCATGCTCGCCCGCTTGGGGT 439
      |||||
Db      1  GCCTCGCCCTCGCCCTCTCTCCGCCCGCTCCCGGT 42

RESULT 24
AUI04419/c
LOCUS   AUI04419          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION AUI04419 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
          HEP22703, mRNA sequence.
ACCESSION AUI04419
VERSION   AUI04419.1 GI:13553940
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS   Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
          EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL   Contact: Yutaka Suzuki
COMMENT   Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yuzuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="COLF1717"
                     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      2.0%; Score 19.6; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.7e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      711  CCAACCAATAGCCCCCCCCCAAGCAGGAC 744
      |||||
Db      37  CTAGCCCATGAGCCTCACCCCTCAAGCAGGAC 4

MATCHES 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy      711  CCAACCAATAGCCCCCCCCCAAGCAGGAC 744
      |||||
Db      37  CTAGCCCATGAGCCTCACCCCTCAAGCAGGAC 4

```


JOURNAL
PUBMED
COMMENT

mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP22703"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 2.0%; Score 19.6; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.7e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 880 GAGGTGACCCACCCAGAGTGTGGCCACGTGGGCAAAACAG 921
|||||
Db 46 GAGGCCGCGATCCAGGATGGCGACGAGTGGCCAAACAG 5
|||||

RESULT 25
AZ859427
LOCUS
DEFINITION
2M0165I06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0165I06 F, genomic survey sequence.

ACCESSION
AZ859427
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: 1 column: 06
Seq primer: CGTTGTAACAGCAGGCCAGT
Class: plasmid ends
High quality sequence stop: 42.

FEATURES
source
Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0165I06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

Qy 939 CTGGTGTCTGCTGCTGCAGGGGTGCAGCAGAGCGGG 975
|||||
Db 6 CTGGGAGTGGAGGGGCTGGGGTGGGGGAGAGCGGG 42
|||||

RESULT 26
CC178199
LOCUS
DEFINITION
XC750 BayGenomics Gene Trap Library pGTLXf Mus musculus CDNA, mRNA
sequence.

ACCESSION
CC178199
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 45)
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XC750
Class: Gene Trap.

FEATURES
source
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTLXf"
/note="Vector: pGTLXf"

ORIGIN
Query Match 1.9%; Score 19.4; DB 9; Length 45;
Best Local Similarity 64.4%; Pred. No. 4e+06;
Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source

1. .40
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1219602"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr22"
/note="Organ: prostate; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Ronaldo."

ORIGIN

Query Match 1.9%; Score 19.2; DB 1; Length 40;
Best Local Similarity 67.5%; Pred. No. 4.4e+06;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 717 AATAAGCCCCCCCCAGCAGGAGACCCCGAGATCA 756

Db 1 AAAGGAACCCCCCCCCAGAAAGACCCCGGTGCCA 40

RESULT 30
AZ359111/c

LOCUS 48 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0101L18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0101L18 R, genomic survey sequence.

ACCESSION AZ359111

VERSION AZ359111.1 GI:10472811

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 48)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0101 row: L column: 18

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 48.

FEATURES

source

Location/Qualifiers
1. .48
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0101L18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.9%; Score 19.2; DB 9; Length 48;
Best Local Similarity 75.0%; Pred. No. 4.7e+06;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 262 ACAGAGACACTCTGCCACCAGCAGCAATATAC 293

Db 41 ACACACACACACACACCCCATCATATATAC 10

RESULT 31

CK151351

LOCUS

DEFINITION

CK151351

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Litopenaeus vannamei (Pacific white shrimp)

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Penaeidea; Litopenaeus.

1 (bases 1 to 49)

Montano-Perez, K., Jimenez-Vega, F., Yepiz-Plascencia, G. and

Vargas-Albores, F.

Litopenaeus vannamei hemocyte subtractive library

Unpublished (2003)

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Email: fvargas@cascabel.ciad.mx

Expressed in Vibrio alginolyticus-inoculated shrimps

Insert Length: 49 Std Error: 0.00

Seq primer: M13R

```

POLYA=No.
FEATURES
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                /db_xref="taxon:6689"
                /cell_type="Hemocyte"
                /dev_stage="adult"
                /clone_lib="Shrimp GS-Vibrio alginolyticus Library"
                /note="Vector: Topo PCR 2.1"
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Best Local Similarity 1.9%; Score 19.2; DB 7; Length 49;
Matches 27; Conservative 1; Mismatches 14; Indels 0; Gaps 0;
Oy 47 CATGGTTCGTCTGCTCTGCAGTCGTCCTCTGGGCTGCTT 88
Db 2 CAAGGTTCTTGGGCTCCGTGGTGGTGGTTCAGGCGCGGTT 43
RESULT 32
CK734037/c
LOCUS
DEFINITION CK734037 49 bp mRNA linear EST 17-FEB-2004
clone TgSTzyk47h09.y1 TGRH Tachyzoite FL CDNA Toxoplasma gondii CDNA
ACCESSION CK734037
VERSION CK734037.1 GI:42587551
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
REFERENCE
AUTHORS Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,D., Wylie,T., Dante,M., Marra,M., Hallier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
TITLE Toxoplasma EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxost@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Putative full length read
vector to vector length is
Seq primer: T7 from Gibco.
FEATURES
    source
        Location/Qualifiers
            1..49
                /organism="Toxoplasma gondii"
                /mol_type="mRNA"
                /db_xref="taxon:5811"
                /clones="TgSTzyk47h09.y1"
                /dev_stage="Tachyzoite"
                /lab_host="GC10"
                /clone_lib="TGRH Tachyzoite FL CDNA"
                /notes="Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; The
                cDNA library was constructed by Keliang Tang, adn Robert
                Cole at Washington University. Total RNA was converted to
                cDNA using the template-switching PCR method (Creator
                SMART cDNA, Clontech, Inc.). First strand was reverse
                transcribed using the CDS III/3' primer and a 5' template
                switch primer using the same primer set and the fragments
                were digested with Sfil. The directional Sfil sites, and
                electroporated into GC10 Competent cells. Antibiotic:
                Chloramphenicol (30ug/ml)"
ORIGIN

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Query Match
Best Local Similarity 1.9%; Score 19.2; DB 7; Length 49;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Oy 596 TGTGTCTGTGGTCCCGAGGATCGGTGAGAG 627
Db 49 TGTGTGTGTGTCGACACAGATCAGCTGAGAG 18
RESULT 33
AUI02702/c
LOCUS
DEFINITION AUI02702 Sugano Homo sapiens cDNA library EST 28-JAN-2004
CAS08541, mRNA sequence.
ACCESSION AUI02702
VERSION AUI02702.1 GI:13552223
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by a fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
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                /clone="CAS08541"
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ORIGIN
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Best Local Similarity 1.9%; Score 19.2; DB 1; Length 50;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Oy 965 GCAGAGCGGGAGCTATGCCAGTCAGTCGCCAGCCCTC 1004
Db 45 GCAGTAGCGGTACCGGTACCCCTTTCAGGCCCGAGTTCCTC 6
RESULT 34
AZ369352/c
LOCUS
DEFINITION AZ369352 39 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0119H19 R, genomic survey sequence.
ACCESSION AZ369352
VERSION AZ369352.1 GI:10483052
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 39)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

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Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0119 row: H column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 39.

FEATURES source

1. .39
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0119H19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.9%; Score 19; DB 9; Length 39;
 Best Local Similarity 81.5%; Pred. No. 5e+06;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 970 AGCGGGAGCTATGCCAGTCAGTCC 996
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 Db 32 AGAGTGGATTATGCCAGTCGTGCC 6

RESULT 35
 AG218322
 LOCUS
 DEFINITION
 Drosophila melanogaster DNA, clone:NP0527-5-1, flanking P{GAWB} transposon insertion, genomic survey sequence.
 ACCESSION
 AG218322
 VERSION
 AG218322.1 GI:22765322
 KEYWORDS
 GSS.

ORGANISM
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1

AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT
 FEATURES
 source

1. 48
 Location/Qualifiers
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /strain="NP0527"
 /db_xref="taxon:7227"
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ORIGIN

Query Match 1.9%; Score 19; DB 10; Length 48;
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 Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 284 GCACAAATATCGACCCCACTAGGCTTCGGG 318
 |||||
 Db 5 GCGCCAAACTTCGACTGCAACCGTGGCATCGCG 39

RESULT 36
 AUI05004
 LOCUS

DEFINITION
 AUI05004 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC07808, mRNA sequence.
 ACCESSION
 AUI05004
 VERSION
 AUI05004.1 GI:13554525
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 11375929

REFERENCE
 AUTHORS

TITLE
 JOURNAL
 PUBMED
 COMMENT

Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 71.4%; Pred. No. 5.4e+06;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 941 GGTGTGCTGCTGCAGGGGTGCAGGCAGAGAGCGGG 975
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Db 11 GGTGGGCTGCTGCAGAGTGGCTGATGCAGAGG 45

RESULT 37
AUI06809
LOCUS
DEFINITION AUI06809 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS03140, mRNA sequence.
ACCESSION AUI06809
VERSION AUI06809.1 GI:13556330
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
        Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
        Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
        Diverse transcriptional initiation revealed by fine, large-scale
        mapping of mRNA start sites
        EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
        Department of Virology
        Institute of Medical Science, University of Tokyo
        4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
        Email: yezuki@ims.u-tokyo.ac.jp
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
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ORIGIN

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Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Db 7 AGACCTAGTGCCTGCTGCTGCTGCAGAGGATCGGCAGGGCAGCG 49

RESULT 39
AUI06812
LOCUS
DEFINITION AUI06812 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HEP23095, mRNA sequence.
ACCESSION AUI06812
VERSION AUI06812.1 GI:13556333
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
        Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
        Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
        Diverse transcriptional initiation revealed by fine, large-scale
        mapping of mRNA start sites
        EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
        Department of Virology
        Institute of Medical Science, University of Tokyo
        4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
        Email: yezuki@ims.u-tokyo.ac.jp
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source Location/Qualifiers
1..50
/mol_type="mRNA"
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ORIGIN

Query Match          1.9%; Score 19; DB 1; Length 50;
Best Local Similarity 65.1%; Pred. No. 5.4e+06;
Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 934 AGACCTGTGCTGCTGCTGCAGGGGTGCAGGCAGAGCGGG 976
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Db 7 AGACCTAGTGCCTGCTGCTGCTGCAGAGGATCGGCAGGGCAGCG 49

RESULT 38
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LOCUS
DEFINITION AUI06811 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            CAS11251, mRNA sequence.
ACCESSION AUI06811
VERSION AUI06811.1 GI:13556332
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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